Title: Perfect score:

Sequence:

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Run on: Š

Scoring table:

Searched:

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Minimum

Database

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Sequence 7, Appli Sequence 31, Appl Sequence 4, Appli Sequence 17, Appli ö Appli Appli Appli Appli Appli Appli Appl Appl Appl Appl Appli Appli Appli Sequence 19, 1 Sequence 19, 1 Sequence 7, Al Sequence 19, 1 Sequence 19, 1 Sequence 19, 1 Sequence 19, 1 Sequence 3, Ap Sequence 3, Ap Sequence 3, Ap Sequence 28, A Sequence 10, 1 Sequence 28, A Sequence 10, 1 Gaps Sequence 49, Sequence 4, 1 Sequence Sequence Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 1 Sequence Sequence Sequence Sequence ö MOLECULES AND METHODS Length 9; Indels Score 55; DB 1; L Pred. No. 2.9e+06; 0; Mismatches 0; PCT-US95-01467-14 PCT-US97-2014411 PCT-US97-2018411 PCT-US98-11189-28 PCT-US98-11189-28 PCT-US98-11189-28 PCT-US98-11189-28 PCT-US99-01188-1 PCT-US99-01188-1 PCT-US99-01188-1 PCT-US99-01188-1 PCT-US99-01188-1 PCT-US99-01188-1 US-08-0018-1 US-08-0018-1 US-08-108-31-7 US-08-108-31-7 US-08-108-31-1 US-08-108-31-1 US-08-108-31-1 US-08-108-31-1 US-08-108-31-1 US-08-443-982-19 US-08-46-7-1 US-08-465-77-8-1 US-08-465-77-8-1 US-08-465-77-8-1 US-08-465-77-8-1 US-08-619-484A-7 US-08-642-120-31 US-08-685-625-4 US-08-690-011-17 US-08-690-011-49 US-08-750-111-4 US-08-756-416-6 US-08-793-076-54 APPLICANT: Washington Unlyersity
TITLE OF INVENTION: NOVEL TRANSDUCTION MOLEC
TITLE OF INVENTION: FOR USING SAME
FILE REFERENCE: 49054-PCT
CURRENT APPLICATION NUMBER: PCT/USOO/05097
CURRENT FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-08-29
PRIOR FILING DATE: 1999-08-29
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 17 ALIGNMENTS CTT-US00-05097-17 ; Sequence 17, Application PC/TUS0005097; GENERAL INFORMATION: 100.0%; Query Match 100.

Best Local Similarity 100.

Matches 9; Conservative 6 1 YPYDVPDYA 9 ORGANISM: Unknown YPYDVPDYA RESULT 1 PCT-US00-05097-17 TYPE: PRT FEATURE: \_ g ò , Appl ; Search time 266.73 Seconds
(without alignments)
9.369 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence 20, Sequence 28, Sequence 43, Sequence 11, A Sequence 10, Sequence 5, A Sequence 6, A Sequence 17, Sequence 9, A Description Pending\_Patents\_AA\_Main:\*

1: \cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep:\*
2: \cgn2\_6/ptodata/2/paa/USO6\_COMB.pep:\*
3: \cgn2\_6/ptodata/2/paa/USO6\_COMB.pep:\*
4: \cgn2\_6/ptodata/2/paa/USO8\_COMB.pep:\*
5: \cgn2\_6/ptodata/2/paa/USO8\_COMB.pep:\*
6: \cgn2\_6/ptodata/2/paa/USO8\_COMB.pep:\*
7: \cgn2\_6/ptodata/2/paa/USO8\_COMB.pep:\*
8: \cgn2\_6/ptodata/2/paa/USO8\_COMB.pep:\*
9: \cgn2\_6/ptodata/2/paa/USO8\_COMB.pep:\*
11: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
11: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
12: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
13: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
14: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
15: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
16: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
17: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
18: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
19: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
21: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
22: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
23: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
23: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\*
23: \cgn2\_6/ptodata/2/paa/USO9\_COMB.pep:\* /cgn2\_6/ptodata/2/paa/US099\_COMB.pep: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:\* 4.5 Compugen Ltd. PCT-US00-05097-17
PCT-US00-19198-20
PCT-US00-19198-20
PCT-US00-20131A-28
PCT-US00-22456-1
PCT-US00-23158-10
PCT-US00-33128-5
PCT-US033-12643-6 Total number of hits satisfying chosen parameters: 3148936 segs, 277657034 residues version -SUMMARIES Minimum Match 0% Maximum Match 100% Listing first 45 summaries protein search, using sw model April 11, 2002, 10:14:10 BLOSUM62 Gapop 10.0 , Gapext 0.5 GenCore Copyright (c) 1993 seq length: 0 seq length: 200000000 US-09-284-787-1 55 DB YPYDVPDYA 9 Length Query Match Post-processing:

Score

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CURRENT FILING DATE: 2000-07-24
                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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PCT-US00-20131A-43
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PCT-US00-22456-1
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                                                           Sequence 9, Application PC/TUS0006950
GENERAL INFORMATION:
BAPLICANT: VALIGENE CORPORATION
TITLE OF INVENTION: METHODS FOR DETECTION OF NUCLEIC ACID POLYMORPHISMS USING
TITLE OF INVENTION: PEPTIDE-LABELED OLIGONUCLEOTIDES AND ANTIBODY ARRAYS
FILE REFERENCE: 9408-042-228
CURRENT APPLICATION NUMBER: PCT/US00/06950
CURRENT APPLICATION NUMBER: PCT/US00/06950
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 9
LENGTH: 9
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GENERAL INFORMATION:
APPLICANT: James S. HUSTON et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS;
FILE REFERENCE: INR-004PC
CURRENT APPLICATION NUMBER: PCT/US00/20131A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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PCT-US00-19198-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Follistatin-3
FILE REFERENCE: PF38BPCT2
CURRENT APPLICATION NUMBER: PCT/USOO/19198
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/144,088
PRIOR FILING DATE: 1999-07-16
NUMBER OF SEQ 1D NOS: 22
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Oryctolagus cuniculus PCT-US00-06950-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
PCT-USO0-19198-20
; Sequence 20, Application PC/TUSO019198
; GENERAL INFORMATION CONOME Sciences, In-
                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Primer_Bind
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                                ULT 2
-US00-06950-9
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
CURRENT APPLICATION NUMBER: PCT/US00/20131A
CURRENT FILING DATE: 2000-07-27
PRIOR FILING DATE: 1999-07-27
RUMBER OF SEQ ID NOS: 45
SOFTWARE: PALCATION VET. 2.0
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: construct PCT-US00-20131A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: construct
PCT-US00-20131A-43
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APPLICANT: Donald J. Buchsbaum
APPLICANT: Buck E. Rogers
APPLICANT: Kurt R. Zinn
APPLICANT: Kurt R. Zinn
TITLE OF INVENTION: Gene Transfer Imaging and Uses Thereof
TITLE REFERENCE: D5836CIPPCT
CURRENT APPLICATION NUMBER: PCT/USOO/22456
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 09/374,972
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 2.9e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 43, Application PC/TUS0020131A; GENERAL INFORMATION:
, APPLICANT: James S. HUSTON et al.
PRIOR APPLICATION NUMBER: 60/146,047
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application PC/TUS0022456 GENERAL INFORMATION:
                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
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0; Gaps

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Length 9;
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APPLICANT: Lok, Si
TITLE OF INVENTION: Cell Surface Display of Proteins by
TITLE OF INVENTION: Recombinant Host Cells
FILE REFERENCE: 99-34
CURRENT APPLICATION NUMBER: PCT/US00/30238
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 5
SSCTWARE: FastSEQ for Windows Version 3.0
SEC ID NO 5
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application PC/TUS9312643
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX.INTERACTING PROTEINS AND
TITLE OF INVENTION: RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55; DB 1; 1
Pred. No. 2.9e+06;
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100.0%; Pred. No. 2.9e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                               CTHER INFORMATION: Hemagglutinin A epitope tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12643
FILING DATE: 29-DEC-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,162
ARR: 00786/160001
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APPLICATION NUMBER: 08/011,398
FILLING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: N/
                                                                                                                                                                                                                                                                                                                                                                                                                              1 YPYDVPDYA 9
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PCT-US93-12643-6
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PCT-US93-12643-6
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GENERAL INFORMATION:
APPLICANT: Cunningham, Sonia
Barros, Maria Pla
TITLE OF INVENTION: A POLYNUCLEOTIDE ENCODING A HUMAN
JUNCTIONAL ADHESION PROTEIN (JAM 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USO0/23158
FILING DATE: 33-Aug-2000
CLASSIFICATION: CURROWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 2.9e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                               100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 2.9e+06;
                                                                                                                                                                                                       Indels
                                                          FEATURE:

COTHER INFORMATION: amino acid sequence of "HA" tag
PCT-US00-22456-1
                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,011 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
PCT-US00-30238-5
PCT-US00-30238-5
Sequence 5, Application PC/TUS0030238
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Katz, Martin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                           TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60601
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PCT-US00-23158-10
    LENGTH: 9
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APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND USES FOR A NOVEL CELL
TITLE OF INVENTION: DEATH PROTECTING PROTEIN
NUMBER OF SEQUENCES: 12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-ELOS/MS-DOS
SOFTWARE: PC-ELOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20344
FILING DATE:
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/15500 FILING DATE: 03.5EP-1997 CLASSIFICATION:
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amin
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PCT-US97-20344-11
; Sequence 11, Application PC/TUS9720344
; GENERAL INFORMATION:
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025,370
FILING DATE: 03-SEP-1996
CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNKNOWN
FILLING DATE: 04-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,:
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: FFASET, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0847;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
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                                                                                           IBM PC compatible
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                 COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERITCS:
LENGTH: 9 amino acids:
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Best Local Similarity 100.

Matches 9; Conservative
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MOLECULE TYPE: protein
PCT-US97-15500-12
                                                                                                            OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS: not
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PCT-US97-20344-11
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GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1080 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
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TITLE OF INVENTION: INHIBITION OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.9e+06;
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BOSILICH, JUNE M.
REGISTRATION NUMBER: 31,238
REFERENCE/POCKET NUMBER: FD-4(
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
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9; Conservative
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CLONE: 12CA5
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; LOCATION: 1..9
PCT-US95-01467-14
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STATE: California
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                                    1 YPYDVPDYA 9
                                                        1 YPYDVPDYA 9
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CITY: Bo
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Length 9; Indels

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APPLICANT: Hall, Frederick L.
APPLICANT: Hall, Frederick L.
APPLICANT: Hall, Erederick L.
APPLICANT: Hall, Erederick L.
APPLICANT: Hall, Bone Morphogenetic
TITLE OF INVENTION: Bone Morphogenetic
TITLE OF INVENTION: Proteins and Their Use in Bone Growth
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABCCHARAL & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 1; I
100.0%; Pred. No. 2.9e+06;
Ative 0; Mismatches 0;
                                                                                                 REGISTRATION NUMBER: 31,071
REGISTRATION NUMBER: 31,071
RELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION NUMBER: PCT/US98/11189
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,966
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PROCA APPLICATION DATA:
PROPLICATION NUMBER: 08/868,452
FILING DATE: 3-June-1997
ATTORNEY/AGENT INFORMATION:
NAME: WOOG, William J.
REGISTRATION UNBER: P-42,236
REFRENCE/DOCKET NUMBER: 30853-11
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US98-11189-28; Sequence 28, Application PC/TUS9811189; GENERAL INFORMATION:
                                                         FILING DATE: 03-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 310-445-114(
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                             LENGTH: 9 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein PCT-US98-06791-1
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: INACTIVATION OF HIV CO-RECEPTORS AS THERAPY
TITLE OF INVENTION: FOR HIV INFECTION
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: PCT/US97/22198
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                                          Length 9;
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GENERAL INFORMATION:
APPLICANT: PORT, J D.
APPLICANT: BRISTOW, MICHAEL R.
TITLE OF INVENTION: "TRANSCENIC MODEL AND TREATMENT FOR TITLE OF INVENTION: HEART DISEASE"
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
                                     100.0%; Score 55; DB 1; 1
100.0%; Pred. No. 2.9e+06;
ive 0; Mismatches 0;
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STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: COLORADO
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 02-DEC-196
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/06791
FILING DATE:
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GENERAL INFORMATION:
APPLICANT:
                                   Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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PCT-US97-22198-1
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Gaps

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; MOLECULE TYPE: protein PCT-US98-11189-28
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Search completed: April 11, 2002, 10:20:50 Job time: 400 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The General Hospital Corporation
APPLICANT: The General Hospital Corporation
APPLICANT: Scadden, David T.
APPLICANT: Lee, Bycong-Chel
TITLE OF INVENTION: METHODS AND PRODUCTS FOR MANIPULATING
TITLE OF INVENTION: HEMATOPOIETIC STEM CELLS
FILE REPRESENCE: M0765/70390/CPRG/KA
CURRENT APPLICATION NUMBER: PCT/US01/45076
CURRENT APPLICATION NUMBER: PCT/US01/45076
CURRENT APPLICATION NUMBER: U.S. 60/250,727
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTESEQ for Windows Version 3.0
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100.0%; Pred. No. 3.1e+05;
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ADDRESSEE: ARIAD Pharmaceuticals, Inc.
US-09-352-171-7
US-09-620-9558-28
US-09-620-9558-43
US-10-001-073-23
US-10-005-15-93
US-10-009-178-10
US-10-009-178-10
US-10-009-178-10
US-10-08-815-7
US-10-08-720-49
US-10-08-720-49
US-10-08-720-49
US-09-56-055A-1
US-09-56-055A-1
US-09-56-055-1
US-09-56-055-1
US-09-645-456-25
US-09-900-590A-28
US-09-900-590A-28
US-09-900-590A-28
US-09-900-590A-28
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GENERAL INFORMATION:
APPLICANT: Crabtree, Gerald R. Schreiber, Stuart L. Spencer, David M. Wandless, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 9, Application PC/TUS0145076
; GENERAL INFORMATION:
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PCT-US01-45076-9
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Best Local Similarity
Matches 9; Conserv
     1 YPYDVPDYA
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US-09-466-568-19
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PCT-US01-45076-9
       SEQ ID NO 9
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       QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17,
Sequence 17,
Sequence 32,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USOG_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
                         version 4.5
- 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-466-568-19
US-09-931-381A-24
US-09-180-167A-17
US-09-175-052A-17
US-09-574-733-32
US-09-574-733-32
US-09-952-370A-33
US-09-975-052-17
US-09-175-052-17
US-09-175-05-17
US-09-175-05-17
US-09-175-05-17
US-09-178-05-18
US-09-18-05-18
US-09-18-05-18
US-09-18-05-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                            GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 2000000000
                                                                                                                                                                                                                                                                  US-09-284-787-1
55
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Maximum DB seq
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                                                                                                                              protein
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2232109877
2443877
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Sequence 9, Application US/09936969
GENERAL INFORMATION:
APPLICANT: IT'S, F.
APPLICANT: POURNY, J.
TITLE OF INVENTION: METHODS FOR DETECTION OF NUCLEIC ACID POLYMORPHISMS USING
TITLE OF INVENTION: PEPTIDE-LABELED OLIGONUCLEOTIDES AND ANTIBODY ARRAYS
FILE REFERENCE: 9408-042-999
CURRENT APPLICATION NUMBER: US/09/936,969
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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) OTHER INFORMATION: Synthetic, based on Orthomyxoviridae Influenza A
) OTHER INFORMATION: virus
US-09-180-167A-17
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Sequence 17, Application US/09180167A

Sequence 17, Application US/09180167A

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

TITLE OF INVENTION: APOPTOSIS

FILE REPERENCE: 50013/004003

CURRENT APPLICATION NUMBER: US/09/180,167A

CURRENT FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: CA 2,198,988

PRIOR FILING DATE: 1997-03-03

PRIOR FILING DATE: 1998-03-02
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                          Indels
100.0%; Pred. No. 3.1e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 5; I
100.0%; Pred. No. 3.1e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Oryctolagus cuniculus
US-09-936-969-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                          9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
                                                                       1 YPYDVPDYA 9
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LENGTH: 9
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GENERAL INCOMMATION:
APPLICANT: Butcher, Eugene C.
APPLICANT: Butcher, Eric J.
APPLICANT: Runkel, Eric J.
APPLICANT: Runkel, Eric J.
APPLICANT: Soler-Ferran, Dulce
TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or:
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or:
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or:
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or:
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or:
TITLE OF INVENTION: 0C810-003
CURRENT FILING DATE: 2000-08-15
PRIOR PILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 24
LEMORTH: 9
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                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 55; DB 5; I
100.0%; Pred. No. 3.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Figg, E. Anthony
REGISTRATION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 2054-114A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/157,753
FILING DATE: -UNKNOWN>
APPLICATION NUMBER: 08,488,653
FILING DATE: 14 -FEB-1995
APPLICATION NUMBER: US 08/478,386
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/466,568
FILING DATE: 17-Dec-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-09-466-568-19
STREET: 26 Landsdowne Street
                      CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 9; Conservative
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US-09-931-381A-24
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Length 9;

DB 5;

100.0%; Score 55;

Query Match

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APPLICANT: Wang, Zhou
APPLICANT: Wang, Zhou
APPLICANT: Wang, Zhou
APPLICANT: Wang, Zhou
APPLICANT: Nang, Wahan
APPLICANT: Nang, Walan
CURENT EFFERENCE: 1720-1-001CIP
CURRENT APPLICANTON NUMBER: US/09/906,393A
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,761
PRIOR FILING DATE: 2000-07-17
APPLICANT: Krols, Luc
TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
FILE REFERENCE: 2283/301
CURRENT APPLICATION NUMBER: US/09/574,735C
CURRENT FILING DATE: 2000-05-18
SOFTWARE: Patentin version 3.0
SEQ ID NO 45
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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APPLICANT: POMECTAIL A.
APPLICANT: POMECTAIL O.
APPLICANT: POMECTAIL O.
TITLE OF INVENTION: Chimeric DNA-binding proteins
FILE REFERENCE: APV-022.02
CURRENT APPLICATION UNMBER: US/09/852,370A
CURRENT PELING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 08/973,131
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1995-12-29
PRIOR FILING DATE: 1994-12-29
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATCHING DATE: 1994-12-29
NUMBER OF SEQ ID NOS: 75
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 55; DB 6; I
100.0%; Pred. No. 3.1e+05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                100.0%; Score 55; DB 6; 1 100.0%; Pred. No. 3.1e+05;
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Best Local Similarity 100.vv
Post 9; Conservative
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                    CRGANISM: HA-epitope
US-09-574-735C-45
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
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APPLICANT: Ward, MIChael
TITLE OF INVENTION: DNA SEQUENCES, VECTORS, AND FUSION POLYPEPTIDES FOR SECRETION OF TITLE OF INVENTION: POLYPEPTIDES IN FILAMENTOUS FUNGI
FILE REPERBNCE: A-62926-1
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 08/785,668
PRIOR FILING DATE: 1997-01-17
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VEFSION 3.1
SEQ ID NO 32
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                                                                                                     APPLICANT DOWGY, Steven F.

TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 4881/1742
CURRENT APPLICATION NUMBER: US/09/775,052A
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/208,966
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTING VET. 2.0
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Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0;
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US-09-574-735C-45
Sequence 45, Application US/09574735C
SERENAL INFORMATION:
APPLICANT: Beeckman, Tom
APPLICANT: Inz,, Dirk
APPLICANT: Van Camp, Wim
                                                                  ; Sequence 17, Application US/09775052A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic. US-09-912-733-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: human
US-09-775-052A-17
                                           US-09-775-052A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-912-733-32
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Alessi, Dario
Cross, Darren
TITLE OF INVENTION: CONTEIN SYNTHESIS, AND SCREENING METHOD
FOR AGENTS
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                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/845,667
FILING DATE: 30-Apr-2001
CLASSIFICATION: <a href="https://documerror.com/lines/lines/lines/">CLASSIFICATION</a>: <a href="https://documerror.com/lines/">CLASSIFICATION</a>: <a href="https://documerror.com/lines/">ADMINISTRATION</a>: <a href="https://documerror.com/lines/">ADMINISTRATION</a>: <a href="https://documerror.com/lines/">ADMINISTRATION</a>: <a href="https://documerro
                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 6; 1
100.0%; Pred. No. 3.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/091,763
FILING DATE: 19-JUN-1998
APPLICATION NUMBER: PCT/GB96/03186
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: GB 9526083.2
FILING DATE: 20-DEC-1995
APPLICATION NUMBER: GB 9610272.8
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: GB 9615066.9
FILING DATE: 18-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENČE ADDRESS:
ADDRESSEE: Braman & Rogalskyj, LLP
STREET: P.O. Box 352
CIT: Canandajqua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-845-667-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09845667
GENERAL INFORMATION:
APPLICANT: Cohen, Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                     ö
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SEQ ID NO 53
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 32
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                                                                                                                                                                     ; OTHER INFORMATION: Peptide US-09-554-726A-53
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 14424-0352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
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Sequence 53, Application US/09554726A

GENERAL INFORMATION:

APPLICANT: HERRANN, Bernhard

APPLICANT: KISPERT, Andreas

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 258,0009 0101

CURRENT APPLICATION NUMBER: US/09/554,726A

CURRENT APPLICATION NUMBER: PG/09/554,726A

CURRENT APPLICATION NUMBER: EP 98/07395

PRIOR APPLICATION NUMBER: EP 98/07395

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-11-18

PRIOR FILING DATE: 1998-11-18

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-03-02

PRIOR FILING DATE: 1998-03-02

WINDER OF SEQ ID NOS: 53

NUMBER OF SEQ ID NOS: 53
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GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF FILE REFERENCE: 4881/1742
CURRENT APPLICATION NUMBER: US/09/775,052
CURRENT FILING DATE: 2001-02-01
PRIOR FILING DATE: 1998-12-10
PRIOR FILING DATE: 1999-12-10
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Pred. No. 3.1e+05;
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100.0%; Pred. No. ...
0; Mismatches
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                                 SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 9
                                                                                                                                                              ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                              ; OTHER INFORMATION: HA Tag
US-09-906-393A-4
      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YPYDVPDYA 9
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US-09-775-052-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-554-726A-53
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                                                                                                                                   TYPE: PRT
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Gaps
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                                                                100.0%; Score 55; DB 6; Length 9; 100.0%; Pred. No. 3.1e+05; ive 0; Mismatches 0; Indels
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                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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    US-09-554-726A-53
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US-09-554-726A-53
Sequence 53, Application US/09554726A
Sequence 53, Application US/09554726A
Sequence 54, Application US/09554726A
Sequence 57, Application US/09554726A
Sevence 57, Application US/09554726A
APPLICANT: KISPERT, Andreas
TITLE OF INVENTION: UNCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATION
TITLE OF INVENTION: THEREOF
FILE REPERENCE: 258,0009 010.
CURRENT APPLICATION NUMBER: US/09/554,726A
CURRENT FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: EP 97 12 0190.0
PRIOR FILING DATE: 1997-11-18
SEQ ID NOS: 53
SOFTWARE: PAGENTION VERSION 3.1
SEQ ID NO 53
LENGTH: 9
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APPLICANT: Church, George
APPLICANT: Church, George
APPLICANT: Das Gupte, Ruchira
APPLICANT: Zhang, Bin
APPLICANT: Schwartz, John
APPLICANT: Lugovskoy, Alexey
TITLE OF INVENTION: MODULAR MOLECULAR CLASPS AND USES THEREOF
TITLE OF INVENTION: MODULAR MOLECULAR CLASPS AND USES THEREOF
TITLE OF INVENTION: MOMBER: US/09/995,847
CURRENT APPLICATION NUMBER: G0/279,524
PRIOR FILING DATE: 2001-01-28
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: HA epitope US-09-995-847-4
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    Length 9;
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                                            Indels
100.0%; Score 55; DB 6; L
100.0%; Pred. No. 3.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                          US-09-995-847-4
Sequence 4, Application US/09995847
GENERAL INFORMATION:
APPLICANT: Rizzuto, Carlo
APPLICANT: Afeyan, Noubar
APPLICANT: Lee, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Peptide
Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                        1 YPYDVPDYA 9
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Title: Perfect score:

Sednence:

protein

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Run on:

Scoring table:

08 08

Minimum Maximum

Database

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APPLICATION TO A STANDARD TO THE TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process TITLE OF INVENTION: Producing the Same and their use FILE REFERENCE: BMID9913US CURRENT APPLICATION NUMBER: US/09/284,787 CURRENT APPLICATION NUMBER: PCT/EP97/05783 PRIOR FILING DATE: 1997-10-20 PRIOR FILING DATE: 1997-10-20 SOFTWARE: Patentin version 3.0
                              Sequence 15, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Apple Sequence 12, Apple Sequence 13, Apple Sequence 13, Apple Sequence 16, Apple Sequence 169, Apple Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 14;
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                                   US-09-459-113A-15

US-09-7459-113A-15

US-08-787-738B-51

US-08-787-738B-51

US-08-787-738B-51

US-08-787-738B-51

US-08-963-368-51

US-08-963-368-6

US-09-108-351-4

US-09-215-69-8

US-09-211-27

US-09-954-043-13

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US-09-954-043-13

US-09-954-043-13

US-09-951-144-8

US-08-592-077-169

US-08-592-077-169

US-08-592-077-169

US-08-592-077-169

US-08-592-077-169

US-08-592-077-169

US-09-921-144-8

US-09-921-144-16

US-09-921-144-16

US-09-921-144-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: human influenza virus
US-09-284-787-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YPYDVPDYAGSGSK 14
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US-09-780-224A-11
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  SEQ ID NO 2
g
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Sequence 11, Appl
Sequence 26, Appl
Sequence 23, Appl
Sequence 25, Appl
                                                                                                                                                   ; Search time 266.73 Seconds
(without alignments)
14.574 Million cell updates/sec
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Sequence 7, Ap
Sequence 7, A
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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Compugen Ltd.
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US-09-780-224A-11
US-09-475-158-56
US-09-622-646-23
US-09-622-646-25
PCT-US00-09002-11
PCT-US08-16887-7
US-09-134-793-7
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                     GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               - protein search, using sw model
                                                                                                                                                        April 11, 2002, 10:20:50
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Gapop 10.0 , Gapext 0.5
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80
1 YPYDVPDYAGSGSK 14
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length: 2000000000
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Match Length
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81.2
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169, App 6, Appl1 8, Appl1

Sequence 2, Appli Sequence 6, Appli Sequence 2, Appli

Appli Appli Appli Appli Appli

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Gaps

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Score

Result è 80 75 67 67 67 65 65

us-09-284-787-2.rapm

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; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence; OTHER INFORMATION: of a fusion protein comprising HA peptide and ; OTHER INFORMATION: C-terminal-lacking soluble HM 1.24 antigenic protein US-09-622-646-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence OTHER INFORMATION: of a fusion protein comprising HA peptide and soluble COTHER INFORMATION: HM 1.24 antigenic protein US-09-622-646-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-02.04 Papel.

US-09-05.24 Papel.

SGERRAL INFORMATION:
APPLICANT: OZAKI, YASUKO
APPLICANT: OZAKI, YASUKO
TITLE OF INVENTION:
MORRENT FOLK MANDER: US/09/622,646
CURRENT APPLICATION NUMBER: US/09/622,646
CURRENT FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: PCT/JP99/00885
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: UP 10-60613
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VOY: 21
SEQ ID NO 2:
LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/09622646
GENERAL INFORMATION:
APPLICANT: OZAKI, YASUKO
APPLICANT: CASHIHARA, YASUKO
TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY
FILE REFERENCE: 053466/0286
CURRENT APPLICATION NUMBER: US/09/622,646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.8%; Score 67; DB 20; Length 143; 78.6%; Pred. No. 0.0084; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 20; Length 126;
Pred. No. 0.0073;
2; Mismatches 1; Indels
       CURRENT APPLICATION NUMBER: US/09/622,646
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/JP99/00885
PRIOR FILING DATE: 1999-02-25
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 23
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78.6%;
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Best Local Similarity 78.6
Matches 11; Conservative
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US-09-622-646-22
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sequence 56, Application US/09475158

sequence 56, Application US/09475158

sequence 56, Application US/09475158

sequence 56, Application Sequence 56, Applicant Gardella, Thomas J.

APPLICANT: Gardella, Thomas J.

APPLICANT: Potts, John T.

APPLICANT: Potts, John T.

TITLE OF INVENTION: PTH Functional Domain Conjugate Peptides, Derivatives

TITLE OF INVENTION: Pheroef and Novel Tethered Ligand-Receptor Molecules

FILE REFERENCE: 0609-478001

CURRENT APPLICATION NUMBER: US/09/475,158

CURRENT FILING DATE: 1999-12-30

PRIOR FILING DATE: 1998-12-31

NUMBER OF SEQ ID NOS: 67

SEQ ID NO 56

LENGHARE: PatentIN Ver. 2.1

SEQ ID NO 56

LENGHARE: 2.1

LENGHARE: 2.1
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Sequence 11, Application US/09780224A
GENERAL INFORMATION:
APPLICANT: Roelvink, Petrus W
APPLICANT: Rovesdi, Imre
APPLICANT: Wickham, Thomas J
TILL OF INVENTION: ADENOVIRAL CAPSID CONTAINING CHIMERIC PROTEIN IX
FILE REFERENCE: 208659
CURRENT APPLICATION NUMBER: US/09/780,224A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,163
PRIOR PILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 11
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US-09-475-158-56
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Sequence 23, Application US/09622646

SEQUENCE INFORMATION:

APPLICANT: OZANY: YASUKO

TITLE OF INVENTION: IMMUNOCHEMICAL ASSAY FOR ANTI-HM1.24 ANTIBODY

FILE REFERENCE: 053466/0286
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100.0%; Pred. No. 0.00047;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 13; Conservative
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ORGANISM: Adenovirus
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Best Local Similarity
Matches 11; Conserv
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US-09-475-158-56
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81.2%; Score 65; DB 1; Length 16;
100.0%; Pred. No. 0.0014;
Live 0; Mismatches 0; Indels
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APPLICANT: Jessee, Joel A.
TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSS:
STREET: DIKe, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                       COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TOWNER: DOWNERS
SOFFWARE: FastESO for Windows Version 2.0
SOFFWARE: PastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 60/056,713
FILING DATE: 22-AUG-1997
ATTORNEY-AGENT INPORMATION:
NAME: CORLESS, PETER F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 4275-PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/056,713
FILING DATE: 22-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09134793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,860
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REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
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        ZIP: 02109
COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CLASSIFICATION:
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                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence; OTHER INFORMATION: of CG M/HA-HM164
US-09-622-646-25
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GENERAL INFORMATION:
APPLICAMY: Mayo Foundation for Medical Education and Research et al.
TITLE OF INVENTION: Anti-apoptotic fusion polypeptide
FILE REFERENCE: 150.195Wol
CURRENT APPLICATION NUMBER: PCT/US00/09002
CURRENT FILING DATE: 2000-0670/128,021
EARLIER APPLICATION NUMBER: US 60/128,021
EARLIER APPLICATION NUMBER: US 60/128,021
EARLIER FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.0087;
2; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Washington University
TITLE OF INVENTION: AND USE THEREOF
GORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/JP99/00885
PRIOR FILING DATE: 1999-02-25
PRIOR PELING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 29
SSOF THAN PRIOR PLING DATE: 1998 COLORS
SSOF THAN PRIOR PALENTIN VET. 2.1
LENGTH: 147
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78.6%;
                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
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PCT-US98-16887-7
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LENGTH: 16
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Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                         RESULT 12
US-09-459-113A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FE
SEQ ID NO 15
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09134793A
GNBEAL INFORMATION:
GNBEAL INFORMATION:
APPLICANT: DOWNY, STEVEN F.
APPLICANT: DOWNY, STEVEN F.
TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM AND USE THEREOF
FILE REPERBENCE: 1142/47275
CURRENT APPLICATION UNMBER: US/09/134,793A
CURRENT FILING DATE: 1998-08-14
SUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Steven F. Dowdy
TITLE OF INVENTION: Methods for Transducing Fusion Molecules
FILE REPRENEUR: 48031
CURRENT APPLICATION NUMBER: US/09/300,639B
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/083,380
PRIOR FILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
EBOGTH: 16
                                                                                                                                                                                                                                          Length 16;
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                                                                                                                                                                                                                                        81.2%; Score 65; DB 15; Length 16
100.0%; Pred. No. 0.0014;
iive 0; Mismatches 0; Indels
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Pred. No. 0.0014;
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
.c.LEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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Best Local Similarity 100.0
.....has 11; Conservative
                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-134-793-7
                                                                                                                                                                                                                                                                                                                               4 YPYDVPDYAGS 14
                                                                                                                                                                                                                                                                                                               1 YPYDVPDYAGS 11
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Best Local Similarity
Matches 11; Conserv
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US-09-134-793A-7
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GEMERAL INFORMATION:
APPLICANT: DOMOY, STEVEN F.
TITLE OF INVENTION: NOVEL TRANSDUCTION MOLECULES AND METHODS FOR USING SAME FILE REFERENCE: 49054(71742)
CURRENT APPLICATION NUMBER: US/09/514,673
CURRENT PAPLICATION NUMBER: 00/0-28
PRIOR FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-02-28
PRIOR FILING DATE: 1999-08-29
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
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GENERAL INFORMATION:
APPLICANT: Steven F. Dowdy
TITLE OF INVENTION: PROTEIN TRANSDUCTION SYSTEM AND METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: 48,884 (1742)
CURRENT APPLICATION NUMBER: US/09/459,113A
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/111,701
PRIOR APPLICATION NUMBER: 60/111,701
PRIOR PILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FRASEQ FOR WINDOWS Version 3.0
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                Length 16;
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           DB 17; Le
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100.0%; Pred. No. 0.0014;
tive 0; Mismatches 0;
81.2%; Scc. 100.0%; Pred. No. v. 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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US-08-708-7388-51
Sequence 51, Application US/08787738B
Sequence 51, Application US/08787738B
GENERAL INFORMATION:
APPLICANT: Notlan, Garry P
TILE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TILLE OF INVENTION: PEPTIDES AND RNA MOLECULES
TILLE REFERENCE: A-64259-1 correction
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 08/589,108
PRIOR PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 17
                                                                                APPLICANT: Notan, Garry P
APPLICANT: Notan, Garry P
APPLICANT: Rothenburg, Michael S.
APPLICANT: Rothenburg, Michael S.
TITLE OF INVENTION: METHIODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-64259-1 correction
CURRENT APPLICATION NUMBER: US/08/787,738
CURRENT APPLICATION NUMBER: US/08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTION NOS: 97
SOFTWARE: PATENTION OF 51
LENGTH: 17
TYPE: PRT
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US-08-787-738-51
Sequence 51, Application US/08787738
GENERAL INFORMATION:
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Search completed: April 11, 2002, 10:20:51 Job time: 401 sec

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Sequence 15, Application US/09775052A; Sequence 15, Application US/09775052A; GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF; FILE REFERENCE: 4881/1742; CURRENT APPLICATION NUMBER: US/09/775,052A; CURRENT FILING DATE: 2001-12-05; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/200,966; PRIOR FILING DATE: 1998-12-10; PRIOR FILING DATE: 1998-12-10; PRIOR FILING DATE: BARLIER FILING DATE: 1997-12-10; NUMBER OF SEQ ID NOS: 57; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
 Sequence Seq
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1.7e-05;
Lna 1; Indels
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Score 71; DB 6;
Pred. No. 3.7e-05
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Grifiths, Andrew
TITLE OF INVENTION: Optical Sorting Method
FILE REFERENCE: 18396/2022
CURRENT APPLICATION NUMBER: US/09/896,915
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: GB9900298.2
PRIOR APPLICATION NUMBER: PCT/GB00/00030
PRIOR APPLICATION NUMBER: PCT/GB00/00030
PRIOR FILING DATE: 2000-01-06
NUMBER: OF SEQ ID NOS: 40
SCOTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 34
TYPE: PRT
TYPE: PRT
TYPE: PRT
CREANISM: plasmid per-23d(FLAGHA)
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92.3%;
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nes 12; Conservative
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   RESULT 2
US-09-775-052A-15
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   Query Match
Best Local Si
Matches 12;
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26.171 Million cell updates/sec
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Sequence 15,
Sequence 51,
Sequence 51,
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Sequence 5
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4: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USOB_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USOS_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USOS_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USOS_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USOS_NEW_COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-775-05215
US-09-976-940-51
US-10-096-550-51
US-09-98-2088-2
US-09-740-876-1
US-09-740-876-1
US-09-626-581C-57
US-09-626-581C-57
US-09-626-581C-57
US-09-626-581C-57
US-09-626-581C-57
US-09-616-581C-57
US-09-616-581C-57
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US-09-616-581C-57
US-09-616-581C-57
US-09-618-581-581
US-10-002-24-13
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US-10-015-535-22
US-10-015-535-23
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US-09-466-568-19
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR

TITLE OF INVENTION: METHODS POR SCREENING FOR TRANSDOMINANT INTRACELLULAR

TITLE OF INVENTION: BFFECTOR BEPTIDES AND RNA MOLECULES

FILE REPERENCE: A -64260-6/RMS/AMS

CURRENT APPLICATION NUMBER: US/09/916,940

CURRENT FILING DATE: 2000-10-28

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1997-01-23

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PATENTIN VET. 2.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Dowly, Steven F.
TITLE OF INVENTION: ANIT-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
TITLE OF INVENTION: ANIT-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
GURRENT APPLICATION NUMBER: 02/09/775,052
CURRENT FILING DATE: 2001-02-01
FRIOR APPLICATION NUMBER: 09/208,966
FRIOR APPLICATION NUMBER: 60/082,402
FRIOR APPLICATION NUMBER: 60/082,402
FRIOR APPLICATION NUMBER: 60/069,012
FRIOR APPLICATION NUMBER: 60/069,012
FRIOR PILING DATE: 1999-012-10
NUMBER OF SEQ 1D NOS: 57
SOFTWARE PATENTING DATE: 1907-12-10
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                                                                                                                                      Length 16;
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                                                                                                                                      Score 65; DB 5; L
Pred. No. 0.00016;
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                                                                                                                                    81.2%; ;
100.0%;
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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                   ; TYPE: PRT
; ORGANISM: human
US-09-775-052A-15
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US-09-775-052-15
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LENGTH: 16
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Sequence 2, Application US/09892208A
GENERAL INFORMATION:
APPLICANT: Goldman, Stanley
APPLICANT: Goldman, Stanley
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
FILE REPERBUES: 18097A-033510US
CURRENT APPLICATION NUMBER: US/09/892,208A
CURRENT FILING DATE: 2001-06-26
FRIOR APPLICATION NUMBER: US 60/214,161
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
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Sequence 51, Application US/10096550

GENERAL INFORMATION:

APPLICANT: Notlan, Garry P

APPLICANT: Notlan, Garry P

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR

TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES

FILE REFERENCE: A-64259-1 correction

CURRENT APPLICATION NUMBER: US/10/096,550

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 08/787,738

PRIOR APPLICATION NUMBER: 08/589,108

PRIOR FILING DATE: 1996-01-23

PRIOR APPLICATION NUMBER: 08/589,911

PRIOR FILING DATE: 1996-01-23

NUMBER OF SEQ ID NOS: 97

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 51
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): LENGTH: 17
): TYPE: PRT
): ORGANISM: Artificial Sequence
): FEATURE:
): OTHER INFORMATION: Description of Artificial Sequence: epitope tag
): OTHER INFORMATION: sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: synthetic. US-10-096-550-51
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                                                                                                                                                                                                                                               81.2%; Score 65; DB 6; Le
100.0%; Pred. No. 0.00017;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 11; Conserv
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Sequence 57. Application US/09415765A
Sequence 57. Application US/09415765A
GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Eustons of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
FILE REFERENCE: A66900-1,FMS/SJR
CURRENT FILING DATE: 1999-10-08
CURRENT FILING DATE: 1999-10-08
FRIOR PILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 19
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                                                             COMPUTER: IMP PC compatible
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/740,876
FILING DATE: 21-Dec-2000
CLASSIFCATION: CUNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/723,726
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: SAVILZKY, MARTINE:
NAME: SAVILZKY, MARTINE:
RECISTRATION NUMBER: 29,699
RECISTRATION NUMBER: 29,699
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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83.3%; Pred. No. 0.0014;
Live 0; Mismatches 2; Indels
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Pred. No. 0.0019;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
02-09-740-876-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (610)454-3816
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
  ZIP: 19426-0997
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 14 amino acids
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83.3%;
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Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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TITLE OF INVENTION: VIRAL VECTORS AND THEIR USE FOR TREATING
HYPERPROLIFERATIVE DISORDERS, IN PARTICULAR RESTENOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUREALL INCORANTION, Stanley
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Maxyen, Inc.
APPLICANT: Whalen, Robert G.
APPLICANT: Whalen, Robert G.
APPLICANT: Waxyen, Inc.
TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
FILE REFERENCE: 18097A-033520US
CURRENT APPLICATION NUMBER: US/10/028,247
CURRENT FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER: US SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                       Score 63; DB 5; Length 86;
Pred. No. 0.0021;
0; Mismatches 2; Indels
                                                                                                             ; OTHER INFORMATION: CotC27 including HAll epitope region US-09-892-208A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: CotC27 including HAll epitope region US-10-028-247-2
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: Mail Drop 3C43, P.O. Box 5093
CITY: Collegeville
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09740876
GENERAL INFORMATION:
APPLICANT: BRANELLEC, Didier
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10028247 GENERAL INFORMATION:
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ISNER, Jeffrey M.
                                                                                                                                                                                                       78.8%;
84.6%;
                                          TYPE: PRT
ORGANISM: Bacillus subtilis
FEATURE:
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Best Local Similarity 84.6
Matches 11; Conservative
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Matches 11; Conservative
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US-09-740-876-1
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SEQ ID NO 2
LENGTH: 86
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Length 14;

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Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 71.4
Matches 10; Conservative
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; LOCATION: (1)..(26)
US-09-481-620A-34
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LENGTH: 27
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US-09-626-580BB-57
US-09-626-580BB-57
Sequence 57, Application US/09626580B
Sequence 57, Application US/09626580B
GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
CURRENT FILING NAMBER: US/09/626,580B
CURRENT FILING DATE: 1908-10-08
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/415,765
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 19
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US-09-626-581C-57
Sequence 57, Application US/09626581C
Sequence 57, Application US/09626581C
Sequence 57, Application:
APPLICANT: Anderson, David
TITLE OF INVENTION: Libraries
TITLE OF INVENTION: Libraries
FILE REFERENCE: A-66900-37RMS
CURRENT APPLICATION NUMBER: 08/09/626,581C
CURRENT PAPLICATION NUMBER: 09/169,015
PRIOR PLICATION NUMBER: 09/169,015
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-626-581C-57
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Pred. No. 0.0019;
0; Mismatches 2; Indels
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83.3%; Pred. No. 0.0019;
Live 0; Mismatches 2; Indels
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.8%;
83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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US-09-481-620A-34
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Sequence 33, Application US/10002244
GENERAL INFORMATION:
APPLICANT: ARIAD Gene Therapeutics, Inc.
TITLE OF INVENTION: Use of Heterologous Transcription Factors in Gene Therapy
FILE REFERENCE: 3468 USC1
CURRENT APPLICATION NUMBER: US/10/002,244
CURRENT FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 68
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APPLICANT: ARIAD Gene Therapeutics, Inc.
TITLE OF INVENTION: Rapamycin Based Regulation of Biological Events
FILE REFERENCE: 345B PCT
CURRENT APPLICATION NUMBER: US/09/481,620A
CURRENT APPLICATION NUMBER: US/09/481,620A
SOFTWARE: PALENT OF SEQ ID NOS: 132
SOFTWARE: PatentIn version 3.0
LENGTH: 26
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US-09-620-9558-31
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Pred. No. 0.002
0; Mismatches
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 12CA5epitope--SV40NLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/09620955B GENERAL INFORMATION:
APPLICANT: Huston, James S.
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.8%;
83.3%;
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71.4%;
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US-09-481-620A-24
; Sequence 24, Application US/09481620A
; General Information:
    TITLE OF INVENTION:
    TITLE OF INVENTION: Rapamycin Based Regulation of Biological Events
; FILE REFERENCE: 345B PCT
; CURRENT APPLICATION NUMBER: US/09/481,620A
; CURRENT PILIO BATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
: LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
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Pred. No. 0.0044;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
COTHER INFORMATION: 12CA5epitope--SV40NLS--ZFHD5/
NAME/KEY: PEPTIDE
LOCATION: (1)..(41)
US-09-481-620a-24
SOFTWARE: Patentin version 3.0

SEQ ID NO 33

LENGTH: 27

TYPE: PRT

ORGANISM: ALLIficial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)

OTHER INFORMATION: PSMTN3
US-10-002-244-33
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Search completed: April 11, 2002, 10:21:36 Job time: 446 sec THIS PAGE BLANK (USPTO)

Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

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APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process
TITLE OF INVENTION: Monoclonal Antibodies Against the Epitope YPYDVPDYA, A Process
TITLE OF INVENTION: Producing the Same and their Use
FILE REFERENCE: BMID9913US
CURRENT APPLICATION NUMBER: US/09/284,787
CURRENT FILING DATE: 1999-08-16
PRIOR APPLICATION NUMBER: PCF/EP97/05783
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 3
                                                 Appli
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                                                                                  Sequence 4, Applysquence 15, Agguence 13, Agguence 13, Agguence 8, Applysquence 8, Applysquence 8, Applysquence 17, Agguence 17, Agguence 17, Agguence 11, Agguence 169, Agguence 169, Agguence 169, Agguence 169, Agguence 169, Agguence 18, Agguence 44, Applysquence 46, 
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                    Sequence 11
Sequence 7,
Sequence 7
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ilarity 100.0%; Pred. No. 2.4e-05;
Conservative 0; Mismatches 0;
US-09-285-912A-68
PCT-US00-09002-11
PCT-US00-09002-11
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-134-793-7
US-09-1459-1138-15
US-09-514-673-15
US-09-514-673-15
US-09-515-693-8
US-09-215-5693-8
US-09-215-5693-8
US-09-215-5693-8
US-09-215-5693-8
US-09-215-5693-8
US-09-215-5693-8
US-09-215-6693-8
US-09-510-169
US-08-591-919-169
US-09-516-065-12
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; ORGANISM: human influenza virus
US-09-284-787-3
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Best Local Similarity
Matches 13; Conserv
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US-08-787-738-51
     LENGTH: 13
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                                                                                                             April 11, 2002, 10:20:51; Search time 266.73 Seconds (without alignments) 13:533 Million cell updates/sec
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Sequence 1
Sequence 2
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-787-738-51
US-08-787-738-51
US-08-963-368-51
US-09-285-912-136
US-09-285-912A-130
US-09-285-912A-130
US-09-285-912A-130
US-09-285-912-130
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                                                                                                                                                                                                                                                                                                   3148936 seqs, 277657034 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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75 67 67 67 67 67

Result No.

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Score 67; DB 13;
Pred. No. 0.00068;
0; Mismatches 1;
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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US-09-285-912A-136
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                                APPLICANT: Notan, Garry P
APPLICANT: Notan, Garry P
APPLICANT: Rothenburg, Michael S.
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-64259-1 correction
CURRENT APPLICATION NUMBER: US/08/787,738
CURRENT APPLICATION NUMBER: 08/589,108
PRIOR PLICATION NUMBER: 08/589,11
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 51
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nolan, Garry P
APPLICANT: Nolan, Garry P
APPLICANT: Nothenburg Michael S.
TITLE OF INVENTION: METHIOSE FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: DEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-64259-1 COLTECTION
CURRENT APPLICATION NUMBER: US/08/787,738B
CURRENT FILING DATE: 1290-01-8
PRIOR FILING DATE: 1990-01-23
PRIOR FILING DATE: 1990-01-23
PRIOR FILING DATE: 1990-01-23
PRIOR FILING DATE: 1990-01-23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 17
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US-08-787-738-51
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US-08-787-738B-51
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Pred. No. 0.00068;
0; Mismatches 1; Indels
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Pred. No. 0.00068;
0; Mismatches 1;
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US-08-787-738B-51
Sequence 51, Application US/08787738B
; GENERAL INFORMATION:
Sequence 51, Application US/08787738 GENERAL INFORMATION:
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; GENERAL INFORMATION:
; APPLICANT: Nolan, Garry P
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91.7%;
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91.7%;
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Best Local Similarity
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Best Local Similarity
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US-08-963-368-51
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TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRA-CELLULAR
FILE REPERBENCE: A-64250-2/DJB/RNS/DR
CURRENT APPLICATION NUMBER: US/08/963,368
CURRENT FILING DATE: 1997-11-03
PRIOR PILICATION NUMBER: 08/589,108
PRIOR PILICATION NUMBER: 08/589,108
PRIOR PLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1997-01-23
NUMBER OF SEQ ID NOS: 102
SCOTUMENT: PARCHILL VOY: 2.0
SCOTUMENT: PARCHILL VOY: 2.0
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TILLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES
TILLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES
FILE REFERENCE: A - 66103 - 1,D19,M8/S,912
CURRENT APPLICATION NUMBER: US/09/285,912
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 136
LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES
FILE REPERENCE: A-66103-11/DJB/RMS/SJR
CURRENT APPLICATION NUMBER: US/09/285,912A
CURRENT FILING DATE: 1999-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: epitope tag OTHER INFORMATION: sequence.
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Pred. No. 0.00073;
0; Mismatches 1; Indels
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Gaps

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APPLICANT: Anderson, David
TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES
FILE REPERENCE: A-66103-1/DJB/RMS/SJR
CURRENT APPLICATION NUMBER: US/09/285,912
CURRENT FILING DATE: 1999-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 0.0018;
0; Mismatches 1; Indels
                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 68, Application US/09285912; GENERAL INFORMATION:
                             89.3%;
91.7%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 91.7
Matches 11; Conservative
                                Query Match 89.3
Best Local Similarity 91.7
Matches 11; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-285-912-68
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LENGTH: 38
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Sequence 130, Application US/09285912
Sequence 130, Application US/09285912
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: PEPTIDES CAUSING FORMATION OF COMPACT STRUCTURES:
FILE REFERENCE: A-66103-1/JOBAPRAS/SSR
CURRENT APPLICATION NUMBER: US/09/285,912
CURRENT APPLICATION NUMBER: 60/080,444
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 130
LENGTH: 37
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                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-285-912A-136
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Pred. No. 0.00073;
0; Mismatches 1; Indels
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91.7%;
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91.78;
                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conservative
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                                                                                           SEQ ID NO 136
LENGTH: 18
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INFORMATION FOR SEQ ID NO:
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   ; MOLECULE TYPE: protein PCT-US98-16887-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DOWDY, STEVEN
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US-09-134-793A-7
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US-09-134-793-7
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               Sequence 11. Application PC/TUS0009002
GENERAL INFORMATION:
FEDERAL INFORMATION:
TITLE OF INVENTION: Anti-apoptchic fusion polypeptide
FILE REFERENCE: 150.195w01
CURRENT FILING DATE: 2000-04.07
EARLIER APPLICATION NUMBER: US 60/128,021
EARLIER FILING DATE: 1999-04-06
EARLIER FILING DATE: 1999-04-05
SEALLER FILING DATE: 1999-04-05
SOFTWARE: FILING DATE: 1999-04-05
SOFTWARE: FILING DATE: 1999-04-05
SOFTWARE: FILING DATE: 1999-04-05
SOFTWARE: FASTER FOR WINDOWS VERSION 4.0
SEQ ID NO 11
LENGTH: 16
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APPLICANT: Washington University
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman,
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 1;
Pred. No. 0.0014;
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47275-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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100.0%; Pred
0; F
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APPLICATION NUMBER: 60/056,713
FILING DATE: 22-AGG-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
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TOPOLOGY: linear
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Best Local Similarity
Matches 11; Conserva
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CLASSIFICATION:
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PCT-US00-09002-11
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PCT-US98-16887-7
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STATE:
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Score 65; DB 1; Length 10,
Pred. No. 0.0014;
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GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
APPLICANT: Jessee, Joel A.
TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 15; L/Pred. No. 0.0014;
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SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,793
   86.7%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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100.0%; Pred. No. v...
... 0; Mismatches
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REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 47:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0:
FILING DATE: 22-AUG-1997
ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 11; Conservative
                 Query Match 86.7
Best Local Similarity 100.
Matches 11; Conservative
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FEATURE:
OTHER INFORMATION: Amino acid sequence of ptat-HA plasmid linker sequence
US-09-300-639B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pTAT-HA linker
US-09-134-793A-7
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| Sequence 4, Application US/09300639B
| Sequence 1, Application US/09300639B
| GENERAL INFORMATION: Methods for Transducing Fusion Molecules |
| TITLE OF INVENTION: Methods for Transducing Fusion Molecules |
| FILE REFERENCE: 48031 |
| CURRENT APPLICATION NUMBER: US/09/300,639B |
| CURRENT FILING DATE: 1999-04-27 |
| PRIOR PRILING DATE: 1998-04-28 |
| NUMBER OF SEQ ID NOS: 8 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| LENGTH: 16 |
| LENGTH: 17 |
| LENGTH: 1
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APPLICANT: JESSEE, JOEL A.

TITLE OF INVENTION: INDUCIBLE REGULATORY SYSTEM AND USE THEREOF
FILE REPERBENCE: 1742/47275
CURRENT APPLICATION NUMBER: US/09/134,793A
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEC ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
SEC ID NO 7
LENGTH: 16
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86.7%; Score 65; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels
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Search completed: April 11, 2002, 10:20:51 Job time: 401 sec

2 SGYPYDVPDYA 12

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Sequence 51, Application US/09916940
GENERAL INFORMATION:
APPLICART: Nolan, Garry P
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
TITLE OF INVENTION: BEFECTOR PEPTIDES AND RNA MOLECULES
FILE REFERENCE: A-64260-6/RMS/AMS
CURRENT FILING DATE: 2001-07-27
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/963,368
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1996-01-23
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Pred. No. 4.2e-05;
0; Mismatches 1;
SQUENCE 8, Application US/09896915
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Griffiths, Andrew
TTPLICANT: Griffiths, Andrew
TTPLE OF INVENTION: OPLICAL Sorting Method
FILE REFERENCE: 18396/2022
CURRENT APPLICATION NUMBER: US/09/896,915
CURRENT FILING DATE: 1999-01-07
PRIOR APPLICATION NUMBER: GB9900298.2
PRIOR APPLICATION NUMBER: GB9900298.2
PRIOR APPLICATION NUMBER: POT/GB00/00030
PRIOR APPLICATION NUMBER: OT/GB0/00030
PRIOR FILING DATE: 12000-01-06
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTLY VERSION 3.1
SEQ ID NO 8
LENGTH: 34
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; ORGANISM: plasmid pET-23d(FLAGHA)
US-09-896-915-8
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Best Local Similarity 92.3
Matches 12; Conservative
   1 SGSGYPYDVPDYA 13
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US-09-916-940-51
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US-09-896-915-8
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-016-940-51

US-09-626-580B-57

US-09-626-580B-57

US-09-775-052A-15

US-09-775-052A-15

US-09-775-052-13

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US-09-453-234-46

US-09-453-234-48

US-09-453-234-82

US-09-453-234-82
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US-09-453-234-72
US-09-453-234-74
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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No.
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Query Match 89.3°
Best Local Similarity 91.7°
Matches 11; Conservative
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US-09-626-580B-57
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TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
TITLE OF INVENTION: PEPTIDES AND NOLECCULES
FILE REFERENCE: A-64259-1 correction
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PATENTIN VET: 2.0
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TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
FILE REFERENCE: A66900-1/RMS/SJR
CURRENT APPLICATION NUMBER: US/09/415,765A
                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: epitope tag
OTHER INFORMATION: sequence.
US-09-916-940-51
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US-10-096-550-51
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        PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: US 08/789,333
PRIOR FILING DATE: 1997-01-23
PRIOR FILING DATE: 1997-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver: 2.0
PRIOR APPLICATION NUMBER: US 08/589,911
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; APPLICANT: Nolan, Garry P
                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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US-09-415-765A-57
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US-10-096-550-51
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Sequence 57, Application US/09626580B
GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Publance of Scaffold Proteins with Random Peptide
TITLE OF INVENTION: Libraries
FILE REFERENCE: A-66900-2/RMS
CURRENT APPLICATION NUMBER: US/09/626,580B
CURRENT APPLICATION NUMBER: 09/169,015
PRIOR PILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 19
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GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION: Libraries
FILE REFERENCE: A-66900-3/RMS
CURRENT APPLICATION NUMBER: US/09/626,581C
CURRENT APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/169,015
PRIOR APPLICATION NUMBER: 09/169,016
PRIOR APPLICATION NUMBER: 09/169,018
PRIOR APPLICATION NUMBER: 09/169,018
PRIOR APPLICATION NUMBER: 09/169,018
PRIOR PRIOR DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 09/169,018
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Pred. No. 0.0001;
); Mismatches 1; Indels
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Pred. No. 0.0001;
0; Mismatches 1; Indels
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION UNMBER: 09/169,015
PRIOR FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 57
LENGTH: 19
                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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Pred. No. 0.013;
0; Mismatches 2; Indels
Length 16;
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86.7%; Score 65; DB 6; L 100.0%; Pred. No. 0.00018; ive 0; Mismatches 0;
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Pred. No. 0.013;
0; Mismatches
                                                                                                                                                                                                 Sequence 36, Application US/09453234

Sequence 36, Application US/09453234

GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Conberg, Nis
APPLICANT: Lonberg, Nis
APPLICANT: Boneharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-12-01
CURRENT FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 36
LEWITH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ValkIrs, Gudars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Biosite biagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SED ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SED ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/09453234; GENERAL INFORMATION: APPLICANT: Buechler, Joe
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
                                         11; Conservative
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OTHER INFORMATION: MI-4L
US-09-453-234-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-453-234-36
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                  Best Local Similarity
Matches 11; Conserv
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    Query Match
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GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 48881/1742
CURRENT PELLIG DATE: 2001-02-01
PRIOR PILLING DATE: 1998-12-10
PRIOR PLILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-04-20
PRIOR FILING DATE: 1998-04-20
PRIOR FILING DATE: 1998-04-20
PRIOR FILING DATE: 1997-12-10
PRIOR FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FALCH OF SEG ID NOS: 57
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GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
TILLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 48891/142
CURRENT FILING DATE: 201-12-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-10
PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
SPIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SOFFWARE: PALCHIN Ver. 2.0
                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-626-581C-57
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Pred. No. 0.0001;
0; Mismatches 1; Indels
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                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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Matches 11; Conserv
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; ORGANISM: human
US-09-775-052A-15
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US-09-775-052-15
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SEQ ID NO 57
LENGTH: 19
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Pred. No. 0.013;
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WESULT 1.

WESULT 1.

SEQUENCE 48, APPLICATION US/09453234

SEQUENCE 48, APPLICATION US/09453234

SEQUENCE 48, APPLICANT: Buechler, Joe

APPLICANT: Valkirs, Gunars

APPLICANT: Cray, Jeff

APPLICANT: Lonberg, Mils

APPLICANT: GenPharm International

TITLE NET 1 BUSSITE DIAGNOSTICS, INC.

APPLICANT: GenPharm International

TITLE REFERENCE: 020015-000110US

CURRENT FILING DATE: 1999-12-01

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 112

SEQ ID NO 48

LENGHH: 224
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APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Cray, Jeff
APPLICANT: Conbergy, Nils
APPLICANT: Gray, Jeff
APPLICANT: Gray, Joff
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
TITLE OF INVENTION: Human Antibodies
TITLE OF INVENTION: 1999-12-01
CURRENT FILING DATE: 1999-12-01
FRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 52
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83.3%;
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83.3%;
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CTHER INFORMATION: M1-21L
US-09-453-234-48
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Best Local Similarity
Matches 10; Conserv
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83.3%; Pred. No. 0.013;
ive 0; Mismatches 2; Indels
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Pred. No. 0.013;
0; Mismatches 2; Indels
                                                                                                                                                              APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Generg, Nils
APPLICANT: Genebarm International
TITLE OF INVENTION: Human Antibodies
TITLE REFERENCE: 020015-0001100S
CURRENT FILIANG DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SENGTH: 224
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GENERAL INFORMATION:
APPLICAMT: Buechler, Joe
APPLICAMT: Valkirs, Gunars
APPLICAMT: Valkirs, Gunars
APPLICAMT: Lonbergy, Nils
APPLICAMT: Lonbergy, Nils
APPLICAMT: Genpharm International
TITLE OF INVENTION: Human Antibodies
TITLE OF INVENTION: Human Antibodies
TITLE REFERENCE: 020015-000110US
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 224
                                                                                                                                 Sequence 44, Application US/09453234 GENERAL INFORMATION:
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83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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ORANISM: HOMO SAPIENS
CTHER INFORMATION: MI-10L
US-09-453-234-46
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CTHER INFORMATION: M1-8L
US-09-453-234-44
                     212 GESYPYDVPDYA 223
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RESULT 15

ORENEAL INFORMATION:

SEQUENCE 76, Application US/09453234

SET SEAL INFORMATION:

APPLICANT: Buechler, Joe

APPLICANT: Buechler, Joe

APPLICANT: Conberg, Mils

TITLE OF INVENTION: Human Antibodes

TITLE OF INVENTION: Human Antibodes

TITLE OF INVENTION: Human Antibodes

CURRENT PILING DATE: 1999-12-01

PRIOR RILING DATE: 1999-12-01

PRIOR APPLICATION NUMBER: US 60/157,415

PRIOR FILING DATE: 1999-10-02

SOFTWARE: PETENT: 112

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Search completed: April 11, 2002, 10:21:36 Job time: 446 sec

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Influenza haemaggl 12CA5 epitope of h Human PAR-2 12CA5

12CA5 epitope of r Murine signalling

Influenza haemaggl Haemagglutinin tag Chimeric adenovira Influenza virus ha Peptide sequence o

Perfect score:

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Max-interacting polypeptide and DNA encoding them - used as anticancer agents and to screen for agents which inhibit cellular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                               Max-interacting protein; plasmid pJG4-5; fusion protein; cancer; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                               AAW50249
AAW48632
                                                                AAW60082
AAW60722
AAW59450
AAW46333
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AAY39621
AAY26291
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AAB10960
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AAB14332
AAY96884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 43; 57pp; English.
                                                                                                                                                                                                                                                                                                                                              AAR56545 standard; Protein; 9 AA
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93US-0011398
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WPI; 1994-264033/32.
Hal epitope tag
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AAR56545;
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Hydrophilic peptid
Epitope for anti-H
Transforming growt
Haemagglutinin epi
pJG4-5 library pla
Purification tag o
Influenza virus ha
10-mer peptide tag
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Viral antigenic ep
HA-epitope tag. S
                                                       ; Search time 53.05 Seconds
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/SIDSB/gcgdata/geneseqp/AA1981.DAT:*
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                  522463 seqs, 74073290 residues
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Listing first 45 summaries
                                         OM protein - protein search, using sw model
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AAW03654
AAR92029
AAW27096
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AAW01162
AAW011651
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Match 1
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Score

Result No.

26484

Haemagglutinin epi HA residues used 1 Influenza hemaglut HA tag, SEQ ID NO: SNP detection meth Influenza haemaggl HA epitope, SEQ ID Haemagglutinin epi Influenza virus HA

Murine signalling Amino acid sequenc Influenza hemagglu

Haemagglutinin epi 12CA5 antibody pep

Influenza virus HA C-terminal influen

Human influenza vi Binding domain of Haemagglutinin epi CTLA 4 VLD CDR loo FLAG peptide from Haemagglutinin ant

HA-tag peptide. U Murine signalling Peptide comprising

AA;

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Sequence

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This sequence represents a viral antigenic epitope of influenza virus hammagalutinin. The DNA sequence encoding this antigen may be included into a modified tobacco mosaic virus (TWV) cost protein gene or a modified movement gene. The modified infectious clone is used to transfect a plant which is then cultured such that the epitope may be recovered from the leaves. The epitope coding sequences are included into the coat protein or movement protein genes such that the translated product contains one or more amino acids immediatly adjacent to the product contains one or more amino acids immediatly adjacent to the product contains one or more amino acids immediatly adjacent to the product contains one or more amino acids immediatly adjacent to the product containing modified movement or coat proteins may be used in the method is esp. used for the production of heterologous proteins. The method is esp used for the production of peptides which cause an antigenic response in mammals, partic, for use in viral vaccines, or for generating a contraceptive immune response. The infectious clones may encode coat proteins for other plant viruses, or proteins conferring protein against insects and diseases.
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Truncated; tobacco mosaic virus; TMV; movement protein; coat protein; frame shift; mutation; in-frame stop codon; antigen; mammal; viral vaccine; contraceptive; immune response; plant virus; insect.
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viral antigenic epitope of influenza virus haemagglutinin (12CA5).
                                    nuclear localization sequence (AAR56544), the B42 acid blob transcriptional activation domain and the HA1 epitope tag is expressed from pJG4-5-1. Mxi (and sense/antisense RNA) can be delivered to e.g. bone marrow as therapeutic agents for cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overprodn. of heterologous peptide in plants via tobacco mosaic virus infection - in which the coat protein gene is modified by insertion of heterologous sequence, partic. for producing viral
                                                                                                                                                                                                                                     ;
0
                    Max-interacting (Mxi) protein fusion protein with the SV40
                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                        Score 55; DB 15;
Pred. No. 4.3e+05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 109; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           AAR78372 standard; peptide; 9 AA.
                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                          100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beachy RN, Fitchen JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigens for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-283768/37.
                                                                                                                                                                                                              Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                             1 YPYDVPDYA 9
                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9521248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-1995;
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                                                                                                                                     Sequence
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                 Matches
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AAR78372
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fast-associating protein with novel death domain, AAT39397), which binds the cytoplasmic region of a Fas receptor, and modulates apoptosis induced by activation of the receptor by ligand binding. DNA encoding the tag is fused to the FADD gene by PCR, downstream of a cytomegalovirus promoter-enhancer in plasmid pcDNA3HA-FADD. The reculting fusion protein is expressed in Escherichia coll and used in an assay to demonstrate in vivo association of FADD protein and Fas receptor via death domains. FADD DNA may be used therapy, and FADD protein or a corresponding antibody may be used to screen for agents modulating FADD pathway cellular functions and Fas-associated apoptosis, for use in therapy of e.g. AIDS, inflammation, leukaemla, myocardial infarction, degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - for
                                                                                                                                                                                                                                                                                               HA-epitope tag; affinity tail; FADD; Fas receptor; binding; Fas-associating protein with novel death domain; apoptosis; gene therapy; antibody; immunoassay; drug screening; diagnostic; AIDS; antiinflammatory; antitumour; cerebroprotective;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FADD protein that binds to cytoplasmic region of Fas receptor identifying inhibitors of Fas-associated apoptosis useful for treating e.g. AIDS, leukaemia, stroke, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This HA-epitope tag peptide has been fused to a FADD protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
100.0%; Score 55; DB 16; 100.0%; Pred. No. 4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 55; DB 17; 100.0%; Pred. No. 4.3e+05;
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 51; 96pp; English.
                                                                                                                                                                        AAW03654 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0443982.
95US-0416379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US02857
                                                                                                                                                                                                                                    22-FEB-1997 (first entry)
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dixit VM, O'Rourke K;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 9; Conserv
                                                              σ
                                                                                                                                                                                                                                                                                                                                                                  neuroprotective
                                                                                                                                                                                                                                                                     AA-epitope tag.
                                                              1 YPYDVPDYA
                                                                                WO9631603-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-1995;
03-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-0CT-1996,
                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                       AAW03654;
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                                Matches
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This peptide comprises an epitope for an anti-haemagglutinin (HA) tag monoclonal antibody. It can be included in the sequence of a recombinant G protein-coupled receptor that is activated superiorly by a synthetic ligand, i.e. a RASSL (see AAW30298 and AAW30299), to facilitate ease of detection and purification. RASSLs are used in a novel method for selectively activating a target cell, providing direct, selective control of cellular proliferation, especially for amplification of transfected cells during gene therapy procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selective activation of target cell expressing modified G protein coupled receptor - allows control of cellular proliferation, especially for amplification of transfected cells in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transforming growth factor-beta activated kinase epitope HA-TAKI.
                                                                                                    Selective target cell activation; G protein-coupled receptor; RASSL; gene therapy; cell proliferation; haemagglutinin; HA tag; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGF-beta; signal transmission; TGF-beta activated kinase; MAPK kinase activator; AMK-1; bone morphogenetic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 18;
100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
                                                                     Epitope for anti-HA tag monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 57; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW27094 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                 97WO-US05334
                                                                                                                                                                                                                                                                                                                                    96US-0622348
                                  14-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein kinase; epitope.
                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-502739/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YPYDVPDYA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP09163990-A.
                                                                                                                                                                                                                                                                                               25-MAR-1997;
                                                                                                                                                                                                                                                                                                                                    26-MAR-1996;
                                                                                                                                                                                                                     WO9735478-A1
                                                                                                                                                                                                                                                                                                                                                                                                              Conklin BR;
                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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AAW30296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides contain a first portion of 5-99 amino acids joined to a second portion contg. at least a functional domain of epimorphin. The first portion may be selected from the peptides 91ven in AAR92029 to AAR92036. The second portion may be full-length epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins). Fragments of epimorphins given in AAT16083 to AAT16090 are used in the produ. of modified epimorphins. The modified epimorphins are useful for the development of diagnosis and treatment of morphogenetic abnormalities of epithelial tissue or novel remedies for wounds, eg burns, after surgery and for artificial organs. They may also be used as components of cosmetics, hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptide containing an epimorphin functional domain - has possible benefits in epithelial tissue treatments, e.g. burns and for artificial organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                   Epimorphin; human; mouse; wound; burn; epithelial tissue; diagnosis; treatment; morphogenetic abnormality; cosmetic; hair growth stimulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                          Hydrophilic peptide for epimorphin modification (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 17; 100.0%; Pred. No. 4.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                             AAR92029 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUME ) SUMITOMO ELECTRIC IND CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 57; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95JP-0099980.
94JP-0162874.
95JP-0099979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95EP-0304270
                                                                                                                                                                                                                       (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koshida S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-118213/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
               1 YPYDVPDYA
                                 31-MAR-1995;
21-JUN-1994;
31-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-1995;
                                                                                                                                                                                                                     29-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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AAW30296

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WO9640767-A2
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                      AAW23660;
                                                                                                                            Sequence
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                                                                                                                                                                                                                                            AAW23660
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                                                                                                                                  The present sequence represents an epitope, HA-TAK1, of transforming growth factor-beta (TGF-beta) activated kinase, TRK-1. The DNA encoding TAK-1 is used to produce the TAK-1 protein which is involved in the TGF-beta family signal transmission system. TAK-1, also known as activator of MAPK Kinase (AMK-1), is an enzyme which is activated kinase by phosphorylation.
                                                                                       DNA encoding transforming growth factor-beta-activated kinase, TAK-1 - useful for studying the TGF-beta signal transmission system
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid binding proteins - having an acidic amino acid sequence extension at the amino-terminus, to increase ability to regulate gene transcription, useful e.g. in cancer therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                               acidic extension peptide; gene control; gene regulation; transcription; dominant negative protein; cancer; drug therapy; drug design; EBP; leucine zipper; haemagglutinin.
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                                                                                                                                                                                                                                                                                                                                                                                                        ONA binding protein; RNA binding protein; amphipathic peptide;
                                                                                                                                                                                                                                    Length 9;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                  ; Score 55; DB
; Pred. No. 4.3¢
0; Mismatches
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                                                                                                                  Example 4; Page 8; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                  AAW00970 standard; Peptide; 9 AA
                                                                                                                                                                                                                                  100.0%; 5
                                           (CHUS ) CHUGAI PHARM CO LTD. (UENO/) UENO N.
                 96US-0685625.
95JP-0253549.
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96JP-0256747
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96us-0018496
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                          Similarity 100.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Haemagglutinin epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krylov D, Vinson CR;
                                                                      WPI; 1997-380171/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-145687/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEA
(VINS/) VINSON C R.
                                                                                                                                                                                                                                                                     1 YPYDVPDYA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRYL/) KRYLOV D.
                                                                                                                                                                                                         9 AA;
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27-SEP-1996;
                 24-JUL-1996;
29-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9705249-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                   AAW00970;
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                    Matches
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The present sequence represents the HAI epitope tag of the pJG4-5 library plasmid used during the isolation of the E6AP-binding proteins. E6AP mediates ubiquitination and so the inactivation of e.g. p53 tumour suppressor. The E6AP-binding protein is likely to be involved in normal cell homeostasis and in the pathogenesis of proliferative and differentiation disorders, e.g. regulation of gene expression or the cell sycle, modification of cell surface receptors, biogenesis of ribosomes and DNA repair. The protein, which can optionally be generated in vivo by gene therapy, may useful in treatment and prevention of papilloma virus infected transformed cells and carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cell differentiation; survival; carcinoma; psoriasis; ubiquitination; p53; tumour suppressor; homeostasis; papilloma virus; epithelial cell; acne; icthyosis; aphthous ulcer; hair growth; antibody; cell proliferation.
                                                                This peptide sequence comprises a haemagglutinin epitope that can be attached to the N-terminus of a nucleic acid binding protein (NABP) such as a leucine zipper bZIP protein or bHith protein.

Claimed NABPs having an appended acidic extension peptide (see AAW00958-65) can regulate the function of a target nucleic acid or gene to which they are bound, and act as potent dominant-negative regulators of gene transcription, cell growth and cell proliferation. They can be used in cancer therapeutics, to treat diseases caused by eukaryotic microorganisms or by viruses, and as tools for drug development, rational drug design, and drug and gene therapies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 55; DB 18;
ilarity 100.0%; Pred. No. 4.3e+05;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pJG4-5 library plasmid HA1 epitope tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rolfe M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 73; 83pp; English.
Claim 16; Page 58; 144pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0484878
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YPYDVPDYA
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and may also be used to regulate epithelial cell processes more generally, e.g. in cases of psoriasis, acne, icthyosis, aphthous ulcers. It may also be used to control wound healing, and inhibit growth of hair. It can also be used to generate antibodies which are used in immunoassays to determine the protein levels. The encoding nucleic acid as be used to prepare recombinant proteins and oligonucleotides useful as probes and primers for diagnostic detection of (mutant) mRNA for the protein in (transformed) cells, also for antisense therapy. It can also be used for the detection of mutations in EGAP-binding protein-encoding genes, mis-expression of these genes or mis-incorporation of the protein assess risk of disorders characterised by cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence represents a specifically claimed purification tag. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prepn. of transforming growth factor-beta fusion protein - useful to reduce surgery recovery time and to prepare artificial skin \,
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                                                                                                                                                                                                                                                                   Length 9;
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                                                                                                                                                                                                                                                                   Score 55; DB 18;
Pred. No. 4.3e+05;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purification tag of a TGF-beta fusion protein.
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                                                                                                                                                                                                                                                                   100.0%;
100.0%;
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Best Local Similarity 100.

Matches 9; Conservative
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HALL F L.
NIMNI M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043065/04.
N-PSDB; AAT42766.
                                                                                                                                                                                                                                                                                                                                  1 YPYDVPDYA 9
                                                                                                                                                                                                                   9 AA;
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1 ypydvpdya
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(NIMN/)
(TUAN/)
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of a purification tag facilitates purification of the fusion protein. The proteinses site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA sequence encoding an influenza virus haemagglutinin (HA) epitope tag (AAM12385) and the murine Ig kappa-chain V-J2-C region signal peptide (AAM12384) was subcloned from a single chain antibody (SFV) contg. vector (pCR3.2) as an ECORV-Sall fragment and ligated with ECORV/Sall-digested pCR3.1.1. The resulting vector was used in the construction of eukaryotic expression vector pPhOx. TM (see also AAT63235). Expression of the HA epitope tag allowed detection of the expressed sFV by monoclonal antibody 12CA5. Vector pphOx.TM is used in novel methods for the identification and isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pPhOx.TM; eukaryotic expression vector; transfected cell; single chain antibody; sFv; molecular hook; haemagglutinin; epitope tag.
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                                                                                                                                                                                            Length 9;
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100.0%; Pred. No. 4.3e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                          100.0%; Score 55; DB 18;
100.0%; Pred. No. 4.3e+05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transfected cells from total cell population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza virus haemagglutinin epitope tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 27; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                      AAW12385 standard; Peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transfected eukaryotic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US15819.
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                                                                                                                                                                                                                           9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bernhard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 9; Conserv
                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conser
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                                                                                                                                                                                                                                                         1 YPYDVPDYA 9
                                                                                                                                              9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Influenza virus.
                                                                                                                                                                                                                                                                           18-JUN-1997
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Best Local S:
Matches 9
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RESULT 12
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                 AAW81556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant antibodies capable of binding to two different antigenic sites, contain Fab fragments from the same or, pref. different antibodies, which are brought into association by complementary antibodies, which are brought into association by complementary interactive domains, esp. leucline zipper domains, which have been inserted into a region of the antibody heavy chain constant region. Recombinant proteins c-fos LZ/Fab OKT2 and c-jun LZ/Fab OKT3 showed ittle or no binding to normal lymphocytes when analysed individually but bound very clearly to the cells when mixed to form a homodimeric antibody. The labelled antibodies are useful for detecting a selected antigen (bound by the first or second Fab) in a biological sample or treatment of cancer and viral infections. AAW01661 is a 10-mer peptide tag derived from Influenza haemagglutinin. DNA encoding the 10-mer was cloned into lambda HC2 to provide a peptide tag which will be present on the heavy chain cloned into pHC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bi:specific antibodies comprising two Fab fragments linked through leucine zipper - useful to detect selected antigen or to treat cancer and viral infections
                                                                                                                                                                                                                                                                                          monoclonal; recombinant; antibody; bispecific; antigenic site;
Fab fragment; complementary interactive domain; leucine zipper;
C-fos; c-jun; treatment; cancer; viral infection; primer; PCR;
polymerase chain reaction; amplification; peptide tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                         10-mer peptide tag derived from Influenza haemagglutinin.
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100.0%; Pred. No. 4.3e+05;
iive 0; Mismatches 0;
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                                                                                                                                             AAW01661 standard; Peptide; 9 AA
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90US-0622983.
91WO-US09019.
94US-0250656.
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Best Local Similarity
9; Conserve
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               1 YPYDVPDYA
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04-DEC-1990;
03-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                AAW01661;
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                                                                                                                         AAW01661
                                                                                                        RESULT
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This represents an in-frame 12CA5 peptide epitope of the alpha chain of mouse leukaemia inhibitory factor (LIF) receptor (LIFR). The invention relates to interspecies LIFR alpha-chain chimeras. The chimeric polypeptide comprises (i) a heemopoietin domain, linked, bound or associated with (ii) an immunoglobulin (Ig)-like domain, such that the chimera can bind cytokines. The chimeric polypeptide specifically binds LIF, so is used to treat conditions that require antagonism of LIF, specifically inflammation, but more generally may be designed to bind other cytokines such as interleukins and colony-stimulating factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Induction; intracellular aggregation; cytoplasmic tail; zeta chain; T cell receptor/CD3 complex; signal; transcription; reporter gene; homodimerization; Fas receptor; cell-specific apoptosis; Gall4; VP16; heterodimerization; primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide containing haemopoietin domain and immunoglobulin-like domain - also related nucleic acid, binds cytokines, specifically leukaemia inhibitory factor, and is used to
                                                                                                                                                                                                  LIFR; leukaemia inhibitory factor; LIF; interspecies; chimeric; haemopoietin domain; immunoglobulin; cytokine; interleukin; colony-stimulating factor; mouse; epitope.
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                                                                                                                                                     12CA5 epitope of mouse LIFR alpha-chain.
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AAW81556 standard; peptide; 9 AA.
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                                                                                                  (first entry)
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Best Local Similarity
The 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treat inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-1998;
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                                                                                                  04-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-1998
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                                                  AAW81556;
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Conservative

1 YPYDVPDYA 9

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This peptide comprises the influenza virus haemagglutinin epitope. A synthetic oligonucleotide (see AAV07684) encoding the epitope has been inserted into plasmid pyun563 (see AAV07705), which contains DNA encoding Mycobacterium tuberculosis recA inteln (see also AAV07705) inserted into an aph selectable marker gene and includes an internal BglII site. E. coli transformants showed a high splicing frequency. The invention provides novel vector constructs that include a DNA sequence encoding an inteln inserted into a selectable marker gene such as aph. DNA of interest can be cloned into a unique restriction site of the inteln, and the vector used as a vaccine or transformed into a vaccine vector. The vectors may also be used in methods of selecting translated open reading frames or genes, leading to the identification of protective antigens of
                                                                                                                                                         New vector constructs for selection of open reading frames - comprise origin of replication and DNA sequences encoding selectable marker, intein and regulatory elements for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemagglutinin 12CA5 epitope; polyclonal rabbit antibody HA.11; human betal-adrenergic receptor; betal-AR; transgene; heart tissue-specific promoter; transgenic animal model; heart muscle disease; heart failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
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                                                    (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
                                                                                                                                                                                                                                       Disclosure; Fig 7; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW80131 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12CA5 epitope of haemagglutinin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                         Daugelat S, Jacobs WR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogenic organisms
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                                                                                                                          WPI; 1998-520797/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bristow MR,
               13-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW76736-W76764 are peptides used to design primers used in a novel method for inducing a biological process in a cell. The method can be used to induce the intracellular aggregation of the cytoplasmic tail of the zeta chain of the T cell receptor/CD3 complex, leading to signalling and transcription of a reporter gene. The method also has applications for the homodimerization of the cytoplasmic tail of the Fas receptor, leading to cell-specific apoptosis and for the heterodimerization of Gall and VP16, leading to direct transcription of a reporter gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing a biological process in a cell using ligand-induced gene expression for e.g. cell death - using DNA construct encoding ligand-binding domain and dimerisable protein domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Intein; reca; DNA repair enzyme; vaccine; vector; antigen; open reading frame; haemagglutinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                       Spencer DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 55; DB 19;
Similarity 100.0%; Pred. No. 4.3e+05;
9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     Crabtree GR, Schreiber SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 71-72; 95pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW66198 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                  ) UNIV LELAND S STANFORD
                                                                                                                                                             95US-0388653.
93US-0017931.
93US-0092977.
94US-0179748.
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94US-0292597
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                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
(STRD ) UNIV LELAND S ST
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV62953.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1998;
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18-AUG-1994;
07-JUN-1995;
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                                                    US5830462-A.
                                                                                                                          07-JUN-1995;
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                                                                                         03-NOV-1998
                                                                                                                                                                                  12-FEB-1993
                                                                                                                                                                                                      16-JUL-1993
                                                                                                                                                                                                                       07-JAN-1994
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The present sequence represents the 12CA5 epitope of haemagglutinin. It is recognised by the polyclonal rabbit antibody HA.11. The sequence was produced by annealing 2 primers encoding the present sequence. These were used to create a epitope tag at the end of human betal-adrenergic receptor (betal-AR) cDNA, which is used to create the transgene of the invention. The specification describes a transgenic animal, especially a mouse, which has incorporated into its genome a transgene comprising a heart tissue-specific promoter operatively linked to a coding sequence comprising betal-LAR, the transgene being expressed in at least the myocardium of the heart of the transgenic animal. The transgenic animal can be used as a model for heart muscle disease and heart failure in a mammal. The transgene can also be used for treating heart failure.
Transgenic mice as models for heart disease - having incorporated in their genome a heart tissue-specific promoter operatively linked to DNA coding for a beta-1-adrenergic receptor
                                                                                                                   Example 1; Page 15; 40pp; English.
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Sequence

ó 100.0%; Score 55; DB 19; Length 9; 100.0%; Pred. No. 4.3e+05; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative 1 YPYDVPDYA 9 ||||||||||||| 1 ypydvpdya 9 QQ δλ

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Gaps

Search completed: April 11, 2002, 10:15:43 Job time: 93 sec

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36, Appl
21, Appl
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19, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFOGRATION:
APPLICANT: ROGET Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
TITLE OF INVENTION: MOLECULES AND METHODS
CORRESPONDENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STRYTE: Massachusetts
CONTYY: U.S.A.
ZIP: O2110-2804
COMPUTER: IBM PS/2 Model 502 or 555X
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/011,398B
FILING DATE: 29 JAN 1993
CLASSIFICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 1.6e+05;
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                   US-08-968-747-12

US-09-156-855-19

US-09-150-855-19

US-08-493-071-21

US-08-158-010-19

US-09-158-010-19

US-09-087-644-3

US-09-087-647-19

US-09-208-966-17

US-09-208-966-17

US-09-100-802-17

US-09-1451-905-38
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PCT-US94-10936-3
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 6, Application US/08011398B; Patent No. 5512473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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  Query Match
  APP11
                                                                                                                                                                                                            (without alignments)
8.190 Million cell updates/sec
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. /cgn2_6/ptodata/2/laa/Ba_COMB.pep:*

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. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*

. /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-170-225-6
US-08-167-08-1
US-08-64-060-31
US-08-461-859-6
US-08-470-837-28
US-08-478-386A-19
US-08-22-267A-60
US-08-922-267A-60
US-08-922-267A-60
US-08-690-011A-17
US-08-690-011A-17
US-08-690-011A-49
US-08-690-011A-49
US-08-690-011A-49
US-08-690-011A-49
US-08-690-011A-49
US-08-690-011A-49
US-08-690-011A-49
US-08-690-011A-49
US-08-690-014-01A-49
US-08-690-014-49
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5-08-483-898-19
5-09-087-716-19
5-08-853-7338-28
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US-08-518-835-6
US-09-157-753-19
US-09-157-230-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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55
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Match Length
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                OM protein
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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                                                                                                                                                                                      Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mastico, Robert Allan
APPLICANT: Stockley, Peter George
TITLE OF INVENTION: CAPSID FORMING AND CYSTEINE
TITLE OF INVENTION: MODIFIED CHIMAERIC MS-2-COAT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 1; I
100.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                            CALT: OALID-2804

CAMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
CONDUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYCTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,038
FILING DATE: 10/30/92
ATOKNEY/ABONT INFORMATION:
NAME: 10/30/92
ATOKNEY/ABONT INFORMATION:
REGISTRATION NUMBER: 30,162
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 10022-4834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44Mb
COMPUTER: IBM Pentium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,982
FILING DATE: 01/03/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08167982 Patent No. 5698424 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Graham & James LLP
STREET: 885 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                            Eish & Richardson
225 Franklin Street
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                    STATE: Massachusetts
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                             COUNTRY: U.S.A.
ZIP: 02110-2804
                                  ALL...
STREET: ...
TTW: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YPYDVPDYA 9
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STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-370-225-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-167-982-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 5580736el Proteins
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Mastico, Robert Allan
APPLICANT: Mastico, Robert Allan
APPLICANT: Stockley, Peter George
APPLICANT: Talbot, Simon John
TITLE OF INVENTION: Antigen-Presenting Capsid with
TITLE OF INVENTION: Pusion MS2-Coat Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rosenman & Colin
STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 1; L
100.0%; Pred. No. 1.6e+05;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
COUNTRY: U.S.A.
ZIP: 10022-2585

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5", 1.44Mb
COMPUTER: IBM PS2-486
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,148
FILING DATE: 08/11/93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9101550.3
FILING DATE: 01/24/91
APPLICATION NUMBER: PCT/GB92/00124
FILING DATE: 01/24/91
APPLICATION NUMBER: PCT/GB92/00124
FILING DATE: 01/22/92
                                                                                                                                                                                                   Sequence 2, Application US/08090148 Patent No. 5534257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08370225
Patent No. 5580736
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Nissenbaum, Israel
REGISTRATION NUMBER: 27,582
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 940-8636
TELEFAX: (212) 940-6404
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                  1 YPYDVPDYA 9
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US-08-370-225-6
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Sequence 6, Application US/08464051
Sequence 6, Application US/08464051
Sequence 6, Application US/08464051
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MOLECULES AND METHODS
INVENTION: MOLECULES AND METHODS
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1519 & Richardson
STREET: 225 Franklin Street
                                                                                             100.0%; Score 55; DB 1; Length 9; 100.0%; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS/Z Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,051
FILING DATE: 05 JUN 1995
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 00786/160002
TELECOMMUNICATION INFORMATION:
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; Patent No. 5786169
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
      ; MOLECULE TYPE: peptide US-08-634-060-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; STRANDEDNESS: N/A; TOPOLOGY: linear US-08-464-051-6
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Patent No. 5712136

GENERAL INFORMATION:

APPLICANT: Wickham, Thomas J.

APPLICANT: Wovesdi, Imre

APPLICANT: Rowesdi, Imre

APPLICANT: ROWENTION: THE ADENOVIRAL WEDIATED CELL TARGETING COMMANDED BY

TITLE OF INVENTION: THE ADENOVIRAL PENTON BASE PROTEIN

NUMBER OF SEQUENCES:

ADDRESSEE: Leydig, Voit 6 Mayer, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Leydly, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: 111nois
COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
APPLICATION NUMBER: UK 9114003.8
FILING DATE: 06/28/91
APPLICATION NUMBER: PCT/GB92/01159
FILING DATE: 06/26/92
ATTORNEY/AGENT INFORMATION:
NAME: Religiold, Jessee
REGISTRATION NUMBER: 20 461
REFERENCE/DOCKET NUMBER: Mastico
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 846-1032
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMM: K114K, John Jr.
REFERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEPHONE: (312) 616-5700
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     AMINO ACID
GY: NOT RELEVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9; Conservative
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         SOFTWARE TO STATE TO SOFTWARE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,386A
FILING DATE: 07/UN/1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: F199, E. Anthony
REGISTRATION NUMBER: 27,195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-478-386A-19
; Sequence 19, Application US/08478386A
; Patent No. 5830462
; Patent No. 5830462
                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/DOS/MS/DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 19:
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-470-837-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
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CITY: Cambridge
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   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tal-Lan
APPLICANT: Tuan, Tal-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
                              APPLICANT: Gyuris, Jeno
APPLICANT: Golemis, Erica
TITLE OF INVENTION: Interaction Trap System for Isolating
TITLE OF INVENTION: No. 5786169el Proteins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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COUNTER INSTANCE ASSACIUSELES
ZIP: 00110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER READABLE FORM:
OPERATING SYSTEM: MS-DOG (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,859
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/370,225
FILING DATE: January 9, 1995
PROFINENT INFORMATION:
APPLICATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
RESIERRENCE/DOCKET NUMBER: 35,238
RESIERRENCE/DOCKET NUMBER: 35,238
RESIERRENCE/DOCKET NUMBER: 35,238
TELEPHONE: (617):542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 28, Application US/08470837; Patent No. 2800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 542-5070
(617) 542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
   Brent, Roger
                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Los Angeles
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-08-461-859-6
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US-08-470-837-28
APPLICANT:
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STATE:
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GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Kleyn, Karen J.
APPLICANT: MOOTE, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
SIREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                           Sequence 6, Application US/08462498
Patent No. 5852169
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
SCHEEDPONDENCE ADDRESS:
ADDRESSE: ALSH & RICHARDSON
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 55; DB 2; Length 9; 100.0%; Pred. No. 1.6e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SUSTWARE: WORDERfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/160001
TELECOMUNICATION INFORMATION:
TELEPAN: (617) 542-5070
TELEFAX: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 60, Application US/08922267A ; Patent No. 5861239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-922-267A-60
                                                                                                                                                                                                                                                                                                                                                  STATE: ME
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                                                                                                                                                                                                Query Match

100.0%; Score 55; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

WEDDUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/292,597
FILING DATE: 18/AUG/1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08292597
Patent No. 5834266
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gerald R. Crabtree
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: And APPLICANT: AND APPLICANTS
ADDRESSE: ARIAD Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
STREET: 26 Landsdowne Street
CITY: Cambridge
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18/AUG/1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTOMBEY/AGENT INFORMATION:
NAME: F199, E. Anthony
REGISTATION UNMBER: 27,195
REFERENCE/DOCKET NUMBER: 2054-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 783-6040
TELERAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
SEQUENCE CHARACTERISTICS
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: 11near
                                                                                            / MOLECULE TYPE: protein US-08-478-386A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-292-597-19
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                                                                               linear
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APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Spencer, David M.
APPLICANT: Mandless, Thomas J.
APPLICANT: Belshaw, Peter
APPLICANT: Gor INVENTION: Other Biological Events
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campholi
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,985
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 55; DB 2; I
; Pred. No. 1.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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APPLICATION NUMBER: US 08/179,748
FILING DATE: 07-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFENCE/DOCKET NUMBER: P-SU 9863
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08473985 Patent No. 5871753
                                             NAME: Figg, E. Anthony
REGISTRATION NUMBER: 27,195
REFERENCE/POCKET UNMBER: 2054
TELECOMMULTAATION INFORMATION:
TELEPHONE: (202) 783-6040
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
illarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 19
                                 ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
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                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-388-653-19
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                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALADA Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,267A
FILING DATE: 2-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,553
FILING DATE: 28-MAR-1997
CLASSIFICATION NUMBER: US 08/829,553
FILING DATE: 12-APR-1996
CLASSIFICATION S30
PRIOR APPLICATION: 530
PRIOR APPLICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REFERENCE/DOCKET NUMBER: 7853-085
TELECOMMUNICATION INFORMATION:
NAME: COLUZZI, LAURA A.
REFERENCE/DOCKET NUMBER: 7853-085
TELECOMMUNICATION INFORMATION:
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SOFTWARE: PECATION BOTA:
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/388,653
FILING DATE: 14-FEB-1995
CLASSIFICATION: 514
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APPLICATION NUMBER: US 08/478,386
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; Patent No. 5869337
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TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 60:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 100.

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STATE: Massachusetts
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Query Match 100.0%; Score 55; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+05; Matches 9; Conservative 0; Mismatches 0; Indels
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MOLECULE TYPE: peptide
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A; Accession: JQ2374
A; Molecule type: mRNA
A; Residues: 1-330 <ROC>
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Listing first 45 summaries
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hemagiutinin - influenza A virus (strain SN1389 and IN0190)
C; Species: influenza A virus
C; Species: 14-011-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C; Accession: J02375; J02376; J023776; J02
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C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C; Accession: J02374
R; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2313-2218, 1193
A; Title: Comparison of 10 influenza A (HINI and H3N2) haemagglutinin sequences
A; Reference number: J02369; MUID:94065682
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hemagglutinin – influenza A virus (strain SN1289)
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A;Residues: 1-330 <ROC>
A;Cross-references: GB:L20119
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
HMIV98
HMIV15
JO1153
JO1154
JO1155
JO1155
HMIVE2
HMIVHA
HM
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A; Molecule type: mRNA
A; Residues: 1-74, Nv, 76-120, Tr, 122-156, Lv, 158-173, Fr, 175-188, Sv, 190-200, Kv, 202-2
A; Residues: 1-74, Nv, 76-120, Tr, 102-156, Lv, 158-173, Fr, 175-188, Sv, 190-200, Kv, 202-2
A; Cross-references: EMBL: 246413; NID: 9609059; PIDN: CAA86548.1; PID: 9609060
A; Experimental source: isolate A/Scotland/142/93
C; Superfamily: influenza virus hemagglutinin
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C.Species: influenza A virus
A;Variety: isolate A/Beijing/333/89
A;Variety: isolate A/Beijing/333/89
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C;Accession: S52174
R;Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circ A;Reference number: S52173
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A; Molecule type: mRNA
A; Residues: 1-74,'N', 74,'N', 122-156,'L', 158-173,'F',175-188,'S',190-200,'K', 202-2
A; Cross-references: EMBL: 246402: NID: 9609041; PIDN: CAA86537.1; PID: 9609042
A; Experimental source: isolate A/England/471/93
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A;Residues: 1-134, K',136-156,'L',158-173,'F',175-188,'S',190-218,'F',220-225,'L',227
A;Cross-references: EMBL:246414; NID:9609061; PIDN:CAA86549.1; PID:9609062
A;Experimental source: isolate A/Scotland/160/93
A;Accession: S52196
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A; Residues: 1-134, K', 136-156, 'L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A; Cross-references: EMBL: 246395; NID: 9609077; PIDN: CAA86530.1; PID: 91228087
A; Experimental source: isolate A/England/269/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-134, K', 136-156, L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A; Cross-references: EMBL: 246399; NID: 9609035; PIDN: CAA86534.1; PID: 9609036
A; Experimental source: isolate A/England/328/93
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A; Residues: 1-134, K', 136-156, L', 158-173, 'F', 175-188, 'S', 190-218, 'F', 220-225, 'L', 227
A; Cross-references: EMBL: 446415; NID: 9609065; PIDN: CAA86550.1; PID: 9609066
A; Experimental source: isolate A/Scotland/174/93
                 A;Cross-references: EMBL:246410; NID:9609053; PIDN:CAA86545.1; PID:9609054 A;Experimental source: isolate A/Hong Kong/23/92 A;Accession: S52192
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A;Residues: 1-347 <ELL>
A;Cross-references: EMBL:246391; NID:g609022; PIDN:CAA86526.1; PID:g609023
A;Experimental source: isolate A/Beijing/353/89
C;Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                              A;Cross-references: EMBL:246409; NID:g609057; PIDN:CAA86544.1; PID:g609058
A;Experimental source: isolate A/Hong Kong/34/90
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                                                                                                                                  A; Molecule type: mRNA
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C.Species: influenza A virus (Insymment)
C.Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C.Accession: S52173; S52190; S52197; S52181; S52196; S52196; S52198
C.Accession: S52173; S52190; S52197; S52181; S52196; S52184; S52193
R.Fellis, J.S.
Submitted to the EMBL Data Library, October 1994
A.Description: Antigenic and genetic variation in the haemagglutinin of recently circula A.Recession: S52173
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A;Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained A;Reference number: JQ2369; MUID:94065682
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C;Species: influenza A virus
C;Date: 14-0ul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: J02378
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained
A;Reference number: J02369; MUID:94065682
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C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: JQ2377
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A;Residues: 1-347 <ELLD.
A;Residues: 1-347 <ELLD.
A;Experimental source: isolate A/Beijing/32/92
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100.0%; Pred. No. 0.022;
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100.0%; Pred. No. 0.022;
ive 0; Mismatches 0; Indels
                                                                                                                                  hemagglutinin - influenza A virus (strain SD0191)
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A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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A; Residues: 1-331 <ROC>
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A; Residues: 1-331 <ROC>
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A,Molecule type: mRNA
A;Residues: 1-347 <ELL>
A;Cross-references: EMBL:Z46396; NID:g609029; PIDN:CAA86531.1; PID:g609030
A;Experimental source: isolate A/England/284/93
C;Superfamily: influenza virus hemagglutinin
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A:Experimental source: isolate A/England/289/93
C:Superfamily: influenza virus hemagglutinin
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S52179
hemaggjutinin - influenza A virus (isolate A/England/286/93) (fragment)
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hemagglutinin – influenza A virus (isolate A/England/289/93) (fragment)
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A;variety: isolate A/England/289/93
C;Date: 07-May-1995 $sequence_revision 23-Feb-1996 $text_change 23-Ma C;Accession: S52180
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin A;Reference number: S52173
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11arity 100.0%; Pred. No. 0.023;
Conservative 0; Mismatches 0
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llarity 100.0%; Pred. No. 0.023;
Conservative 0; Mismatches 0
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Best Local Similarity
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A; Residues: 1-347 <ELL>
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Matches 9
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A:Variety: isolate A/England/247/93.
C. Accession: S52176
Fig. 150.
Fig. 150
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C;Species: influenza A virus
A;Variety: isolate A/England/284/93
A;Variety: isolate A/England/284/93
C;Datc. 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: 552178
R;Ellis, J.S.
R;Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Accession: 552173
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0.023;
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Pred. No. 0.023;
; Mismatches 0
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Pred. No.
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hemagglutinin - influenza A virus (isolate A/England/68/94) (fragment)
C;Species: influenza A virus
C;Species: influenza A/England/68/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52186
C;Accession: S5218
A;Bescription: Antigenic and genetic variation in the haemagglutinin of recently circ
A;Bescription: Antigenic and genetic variation in the haemagglutinin of recently circ
A;Bescription: Antigenic and genetic variation in the haemagglutinin of recently circ
A;Bescription: Antigenic and genetic variation in the haemagglutinin of recently circ
A;Bescription: Associate A/England/68/94
C;Superfamily: influenza virus hemagglutinin
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100.0%; Score 55; DB 2; 100.0%; Pred. No. 0.023;
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Job time: 126 sec
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                               Best_Local Similarity
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                     C; Species: influenza A virus
A; Variety: isolate A/England/328/93
A; Variety: isolate A/England/328/93
C; Date: O'May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C; Accession: S52182
B; Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: S52183
A; Accession: S52182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hemagglutinin - influenza A virus (isolate A/England/347/93) (fragment)
C;Species: influenza A virus
C;Species: influenza A virus
A;Varlety: isolate A/England/347/93
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52183
B;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Reference number: S52173
A;Accession: S52183
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R; Ellis, J.S.
Rsubmitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: $52173
A; Accession: $52185
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A; Residues: 1-347 <ELL>
A; Cross-references: EMBL: Z46401; NID: 9609039; PIDN: CAA86536.1; PID: 9609040
A; Experimental source: isolate A/England/347/93
C; Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                                                                                               PIDN:CAA86535.1; PID:g609038
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A; Residues: 1.347 <ELL.
A; Cross-references: EMBL: Z46403; NID: g609043; PIDN: CAA86538.1; PID: g609044
A; Experimental source: isolate A/England/67/94
C; Superfamily: influenza virus hemagglutinin
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   - influenza A virus (isolate A/England/328/93) (fragment)
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100.0%; Score 55; DB 2; Length 347;

Best Local Similarity 100.0%; Pred. No. 0.023;

Matches 9; Conservative 0; Mismatches 0; Indels
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A; Residues: 1-347 <ELL>
A; Residues: 1-347 <ELL>
A; Cross-references: EMBL:246400; NID:g609037; PI
A; Experimental source: isolate A/England/346/93
C; Superfamily: influenza virus hemagglutinin
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA Gething M.-J., Bye J., Skehel J.J., Waterfield M.;

RA Gething M.-J., Bye J., Skehel J.J., Waterfield M.;

RT "Cloning and DNA Sequence of double-stranded copies of haemagglutinin RT "Cloning and DNA Sequence of double-stranded copies of haemagglutinin RT "Gething M.-J.) Bye J., Skehel J.J., Waterfield M.;

RT "Cloning and DNA Sequence of double-stranded copies of haemagglutinin RT "Gething M.-J.) Bye DNA Sequence of double-stranded copies of haemagglutinin RT "Gething M.-J., Waterfield M.;

RT. "Human influenza virus.";

RL "Autre 287:301-306(1980).

CC -1- FUNCTION: HEWAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CC LOS THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.

CC -1- SUBLINARTY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

DR PIR; A04051; MINVH.

DR HSSP; P03437; SHMG.

INTEAPRO: IPRO01346; Hemagglutin.

DR HSSP; P03477; SHMG.

INTEAPRO: IPRO01364; Hemagglutin.

DR Pfam; PF00509; Hemagglutin; I.

DR Pfam; PF00509; Hemagglutin.

DR Pfam; PF00509; Hemagglutin; I.

DR Pfam; Pf00509; Hemagglutin; I.
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                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN)
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                                                                                                                                                                                                                                   Influenza A virus (strain X-31).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
NCBI_TaxID=11489;
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Copyright (c) 1993 - 2000 Compugen Ltd
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HEMA_IAQU7
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-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                  SEQUENCE FROM N.A. MEDDMed=6164798; Sleigh M.J.; Both G.W., Underwood P.A., Bender V.J.; Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; Mattigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral
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                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ (CONTAINS: HEMAGGLUTININ HAI CHAIN) (FRAGMENT).
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13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAI CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 55; DB 1; Length 328; 100.0%; Pred. No. 0.013;
                                                                                                        Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Influenza virus A and B group; Influenza A viruses;
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                                                                                              Influenza A virus (strain A/England/878/69).
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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38 N-1
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                                       Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
"Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral antigenicity.";
J. Virol. 37:845-853(1981).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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Both G.W., Sleigh M.J.;
"Conservation and variation in the hemagglutinins of Hong Kong
subtype influenza viruses during antigenic drift.";
J. Virol. 39:663-672(1981).
-:- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
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Envelope protein; Hemagglutinin; Glycoprotein
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                     MEDLINE-81194918; PubMed-6164798;
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Pfam; PF00509; Hemagglutinin; 1.
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Matches 9; Conserv
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                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
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SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINNED BY A DISULFIDE BOND.
            SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                          HEMAGGLUTININ HAI CHAIN.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                       SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEMA_IADH1 STANDARD; PRT; 550 AA.
P12582; 084021; 084022;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 14), Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza A virus (strain A/Duck/Hokkaido/5/77).
Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                                                                                                         InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutinin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
I 1 1 CHAIN
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                                                                                                                                                                   EMBL; J02092; AAA43182.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                              61699
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                  A04052; HMIV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-11357;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- SUBUNIT: HOMOTRIBMER, EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LIRKED BY A DISULFIDE BOND.
-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                                 HEMAGGLUTININ HA1 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
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MEDLINE-37265458, PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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12583; Q84011;
01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza A virus (strain A/Duck/Hokkaido/8/80).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7E7ACFE716FC969A CRC64;
                                                                                                                                                        InterPro; IPR001364; Hemagglutn.
Probom; PF00509; Hemagglutinin; 1.
Probom; PD000225; Hemagglutinin; 1.
Prolope protein; Hemagglutinin; Glycoprotein.
NON_TER
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΜW.;
                                                                                                                                            EMBL; M16737; AAA43143.1; -.
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550
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1165
483
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza A virus.
NCBI_TaxID=11358;
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22
38
165
285
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N-LINKED (GLCNAC. . .) (POTENTIAL) 6C30BF67CFDCB7DE CRC64;

61577 MW;

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550 AA;
CARBOHYD
SEQUENCE
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SEQUENCE
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HEMA_IADH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ducks.
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-I- SUBUNIT: HOMOTRINER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISSULFIDE BOND.
-I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                               Gaps
                                                                        N-LINKED (GLCNAC. .) (POTENTIAL).
X-LINKED (GLCNAC. .) (POTENTIAL).
X-N (IN PIR DATA BANK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
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0
                                                                                                                                                                                                                                                                     Similarity 100.0%; Score 55; DB 1; Length 550; Similarity 100.0%; Pred. No. 0.023; 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | HEMA_IADH3 | STANDARD; | PRT; 550 AA. |
| 191584, 084012; 089793; | 01-0CT-1999 (Rel. 12, Created) |
| 101-0CT-1999 (Rel. 12, Last sequence update) |
| 102-0CT-1999 (Rel. 40, Last annotation update) |
| 102-0CT-1999 (Rel. 40, Last annotation update) |
| 103-0CT-1999 (Rel. 40, Last Annotation update) |
| 103-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus (strain A/Duck/Hokkaido/33/80).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                               LINKED (GLCNAC. . .) (P
-> N (IN PIR DATA BANK)
A107023ACC9CC353 CRC64;
                                      HEMAGGLUTININ HAI CHAIN. HEMAGGLUTININ HAZ CHAIN.
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PIR; C27813; HMIV33.
InterPro; IPR001364; Hemagglutn.
Fam; PF00509; Hemagglutnin; 1.
ProDom; PD00025; Hemagglutnin; 1.
Envelope protein; Hemagglutnin; 31.
CHAIN 1328 HEMAGGLUTININ HAI
  protein; Hemagglutinin; Glycoprotein.
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550
22
38
38
285
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8
22
38
165
285
483
137
550 AA;
                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11359;
                                                                                                                                                                                                                                                                                                                                                    1 YPYDVPDYA 9
                                                      CHAIN
CARBOHYD
CARBOHYD
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CARBOHYD
  Envelope
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CARBOHYD
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CARBOHYD
                NON_TER
CHAIN
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HEMA_IADH3
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Matches
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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| 1912867, 084013; 084014; 084014; 01-0CT-1989 (Rel. 12, Created) |
| 101-0CT-1989 (Rel. 12, Last sequence update) |
| 101-0CT-1989 (Rel. 12, Last sequence update) |
| 102-0CT-1989 (Rel. 140, Last annotation update) |
| 102-0CT-1989 (Rel. 140, Last annotation update) |
| 103-0CT-1711 
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100.0%; Score 55; DB 1; Length 550. 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza A virus (strain A/Duck/Hokkaido/7/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Envelope protein; Hemagglutinin; Glycoprotein.
NON_TER 1
                                                                                0; Mismatches
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InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
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                                                                                    Conservative
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Best Local Similarity
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550 AA;
Query Match
Best Local Similarity
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HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HA2 CHAIN) (FRAGMENT).
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PIR; G27813; HMIV15.
InterPro.; IPRO01364; Hemagglutn.
Pfam; PF00509; Hemagglutinln; 1.
ProDom; PD000225; Hemagglutn; 1.
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Matches 9; Conservative
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                                                                                            NCBI_TaxID=11363;
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P43257;
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CARBOHYD
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SEQUENCE
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HEMA_IADHK
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                                                                                                                                                                                                                                                                                                                 Gaps
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N'LINKED (GLCNAC. .) (POTENTIAL).
Y -> N (IN PIR DATA BARK).
W; 67BCD85F44736CFE CRC64;
                                                                                                                                                                                                                                                                    MEDLINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                               HEMA_IADH6 STANDARD; PRT; 550 AA.
P12587; Q84017;
01-0CT-1989 (Rel. 12, Created)
01-0T-1-PR-1990 (Rel. 14, Last sequence update)
20-ARG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                                                                                                                          Influenza A virus (strain A/Duck/Hokkaido/9/85).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00509; Hemagglutinin; 1.
Probom; PD00025; Hemagglutin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
NON_TER 1 328 HEMAGGLUTININ HAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMA_IADH7 STANDARD; PRT; 550 AA. P1258B; Q84018; Q89470; O1-OCT-1989 (Rel. 12, Created) COT-1989 (Rel. 12, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
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X
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550 AA;
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                                       RESULT 9
HEMA_IADH6
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HEMA_IADH7
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                                                                                                                                                                                                                                                                                                                                                                                                                       VILLOGY, 159:109-119(1987).

-!- FUNCTION: HEWAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-!- SUBUNIT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                   MEDIINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza A virus (strain A/Duck/Hong Kong/7/75).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Vifluenza virus A and B group; Influenza A viruses;
Influenza A virus.
Influenza A virus (strain A/Duck/Hokkaido/10/85).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMAGGLUTININ HAI CHAIN. HEMAGGLUTININ HAZ CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Envelope protein; Hemagglutinin; Glycoprotein.
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
           Yasuda J., Shortridge K.F., Shimizu Y., Kida H.; "Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged."; J. Gen. Virol. 72:2007-2010(1991).

-i- FUNCTION: HEMAGGLUTTHIN IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                   -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91341491; PubMed=1875195;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-:- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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P43258;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
02-NOG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN; HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                         HEMAGGLUTININ HAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55;
MEDLINE-91341491; PubMed-1875195;
                                                                                                                                                                                                                                                             EMBL; D00929; BAA00769.1; -.
HSSP; P03437; 5HMG.
InterPro; IPR001364; Hemagglutn.
                                                                                                                                                                                                                                                                                                    Pfam: PF00509; Hemagglutinin; 1. ProDom; PD000225; Hemagglutn; 1.
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550 AA;
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CARBOHYD
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CHAIN
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HEMA_IADHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
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                        SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
00-NG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HA2 CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza A virus (strain A/Duck/Hong Kong/231/77).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutinin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
1 1 1 HEMAGGLUTININ HAI
AND HA2) LINKED BY A DISULFIDE BOND.
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P43259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL RECEPTORS AND FOR INITIATING INFECTION.

-!- SUBUNIT: HOMOTRIBER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISQLEIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88306236; PubMed-3407150;
Katz J.M., Webster R.G.;
"Antigenic and structural characterization of multiple subpopulations
of H3N2 influenza virus from an individual.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 165:446-456(1988).
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                                                  GLCNAC. . .) (POTENTIAL)
9A1E094DA28BACD2 CRC64;
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                        100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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550 AA
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                                                                                                                                                                            Best Local Similarity
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                                                                                                                                    HEMAGGLUTININ HAI CHAIN.
HEMAGGLUTININ HA2 CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
W-LINKED (GLCNAC. . . ) (POTENTIAL).
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza A virus (strain A/Goose/Hong Kong/10/76).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00509; Hemagglutinin; 1.
Probom; PD000225; Hemagglutinin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
CMN_TER 1 1 1 CHAIN
                                                                                                 Envelope protein; Hemagglutinin; Glycoprotein.
NON_TER 1 1 1 1 CHAIN HEMAGGLUTININ HAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          550 AA
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   or send an email to license@isb-sib.ch).
                                                  InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1. Probom; PD000225; Hemagglutn; 1.
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                                  EMBL; D00932; BAA00772.1;
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Best Local Similarity 100.
Matches 9; Conservative
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(POTENTIAL)

SQ SEQUENCE 550 AA; 61804 MW; 52C9F14B309310ED CRC64;

0; Gaps Query Match 100.0%; Score 55; DB 1; Length 550; Best Local Similarity 100.0%; Pred. No. 0.023; Matches 9; Conservative 0; Mismatches 0; Indels

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Search completed: April 11, 2002, 10:22:00 Job time: 430 sec

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STRAIN-TOKYO1537, TOKYO1511;
A MOIT S., Sekine H.; Tokyo1511;
T "HAI domain of Influenza A (H3N2) virus.";
L Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB013807; BAA77285.1; -...
InterPro; IPR001364; Hemagglutin.
P fam: PPR00509; Hemagglutin.i.
R PRINTS; PR00329; HEMAGGLUTR12.
R PRINTS; PR00325; Hemagglutin; 1.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID=11320;
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                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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A Mori S., Sekine H.;
Mori S., Sekine H.;
Mori S., Sekine H.;
L Submitted (MAY 1998) to the EMBL/GenBank/DDBJ databases.
L Submitted (MAY 1998) to the EMBL/GenBank/DDBJ databases.
R EMBL; AB013819; BAA77281.1; ...
R EMBL; AB013819; BAA77287.1; ...
R EMBL; AB013811; BAA77289.1; ...
R EMBL; AB013812; BAA77289.1; ...
R EMBL; AB013812; BAA77289.1; ...
R INCEPPO: IPRO01364; Hemagglutn.
R PF00509; Hemagglutinin; 1.
R PINTYS; PR00329; HEMAGGLUTNIL: 1.
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"Hal domain of Influenza A (H3N2) virus.";
"Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB014062; BA477294.1; -..
REMBL; AB013808; BA477292.1; -..
REMBL; AB014060; BA477292.1; -..
REMBL; AB014061; BA477293.1; -..
RICTEPTO: IPR001364; Hemagglutn.
R Pfam; PF00509; Hemagglutn.
R PRINTS; PR00329; HEMAGGLUTN12.
                                                      Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAIN=72, 70, AND 71;
Nagashima M., Moril S., Sekine H.;
"Influenza A virus gene for hemagglutinin.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                             26493 MW; 457455682C8D28D7 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLITININ (FRAGMENT).
Influenza A virus.
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Last annotation update)
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Matches 9; Conservative
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=A/TAIWAN/2192/96;
Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                        influenza A virus (A/Taiwan/2034/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID-95240;
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                  100.0%; Score 55; DB 12; Length 236; 100.0%; Pred. No. 0.05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139937; AAD34854.1; -.
InterPro: IPR001364; Hemagglutn.
Pfam; PPR0039; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AFG139936; AAD34853.1; -
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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Best Local Similarity 100.
Matches 9; Conservative
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286 AA;
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57 YPYDVPDYA 65
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMENT).
Influenca A virus (AFfinland/583/98(H3N2)).
Viruses; SSRNA negative-strand viruses; Orthomyxoviridae;
Influenca virus A and B group; Influenca A viruses; Influenca A viruse.
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yeacine 0:0-0(2001).
EMBL; AF311689; AAG47810.1; -.
InterPro; IPR001364; Hemagglutn.
PRIMTS; PR00329; HEMAGGLUTN12.
PRIMTS; PR00329; HEMAGGLUTN12.
PRODOM; PR00125; Hemagglutn; 1.
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Kinnunen L.;
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100.0%; Score 55; DB 12; Length 325;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;
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1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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100.0%; Pred. No. 0.073;
tive 0; Mismatches 0;
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EMBL; AF008782; AAB63719.1; -1 nte-Froz. IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutinin; 1. ProDom; PD000225; Hemagglutn; 1.
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STRAIN-A/FINLAND/583/98;
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Best Local Similarity
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SEQUENCE FROM N.A.
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STRAIN-A/TRIMWA/2191/96;
Shih S.-R., Chen S.-H., Wu S.-L., HO C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                influenza A virus (A/Talwan/2191/96(H3N2)).
Virusas: ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95236;
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Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID-11320;
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STRAIN=A/ILLINOIS/S/95(H3N2);
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF139932; AAD34849.1; -. InterPro: IPR001364; Hemagglutn. Pfdm; PF005099; Hemagglutin. 1. PRINTS; PR00329; HEMAGGLUTN12. ProDom; PD000225; Hemagglutn: 1.
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                                                  286
32059 MW; CB51B092AAD0D7D8 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Best Local Similarity 100.
Matches 9; Conservative
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286 AA;
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"Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza season."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, PR087700; AAC36729.1; ...
InterPro; IPR001364; Hemagglutn.
Probom; PD000225; Hemagglutnin; 1.
Probom; PD000225; Hemagglutn; 1.
NON_TER 327
SEQUENCE 327 AA; 36389 MW; 909239953649069E CRC64;
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EMBL; AF087703; AAC36732.1; - InterPro: InterPr
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Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID=11320;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID=11320;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Osiowy C.K.;
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Best Local Similarity 100.0
Matches 9; Conservative
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-A/PENNSYLVANIA/7/94(H3N2);
STRAIN-A/PENNSYLVANIA/7/94(H3N2);
Strain-A-A-Benns R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF008788; AAB63725.1;
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutnin; 1.
ProDom; PD000225; Hemagglutn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses. NCBL_TaxID=11320;
                   Fitch W.M., Bush R.M., Bender C.A., Cox N.J.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF0008797; AAB63724.1.; InterPro; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutin. 1. ProDom: P000025; Hemagglutinin; 1. NON_TER
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326 326 MW; 4B84BD4AADC44A77 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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STRAIN=A/NEW_YORK/28/94 (H3N2);
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Best Local Similarity 100.
Matches 9; Conservative
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326 AA;
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                                OSIOWY C.K.;
"Genefic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
"Genefic characterization of A/Sydney/05/97-like(H3N2) Influenza season.";
"Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC87709; AAC36738.1; -.
Interpro; IPR001364; Hemaggluttn.
Pfam; PF00509; Hemaggluttn.h.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus isolates circulating in Canada during the 1997/98 Influenza season."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF087701; AAC36730.1; Henagglutn.
InterPro: IPR001364; Henagglutn.
Pfam; PF000099; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
PRODOM; PD000225; Hemagglutn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          influenza A virus (A/Sydney/05/97-like(H3N2)).
Virusas; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID=82372;
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                                                                                                                                    327 AA; 36373 MW; ADBD67D856EBCC96 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMENT).
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STRAIN-A/SYDNEY/05/97-LIKE(H3N2);
                      STRAIN-A/SYDNEY/05/97 (H3N2);
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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Q9YT89;
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09YT89
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os influenza A virus (A/Sydney/O5/97-11ke(H3N2)).

Oc viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OX NCBI_TaxID=82372;
RN (1)

RP SEQUENCE FROM N.A.

RS STAIN-A/SYDNEY/O5/97-LIKE(H3N2);
RA OSIOWY C.K.;
RT Genetic characterization of A/Sydney/O5/97-like(H3N2) Influenza virus
RT Solates circulating in Canada during the 1997/98 Influenza virus
RT Solates circulating in Canada during the 1997/98 Influenza virus
REMBL, AFO00702; Hemagglutin. 1.
DR PRINTS; PRO0329; Hemagglutin. 1.
FT NON_TER 327 327
SQ SEQUENCE 327 AA; 36446 MW; 9E9FA8433CFC1B01 CRC64;

OUETY MATCh
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
OY 1 YPYDVPDYA 106
DP 98 YPYDVPDYA 106
Search completed: April 11, 2002, 10:22:57
30b Lime: 427 sec
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Haemagglutinin seq Haemagglutinin tag Expression vector pHOOK-1.GM-CSF fus Anti-Fc gamma rece Anti Fc alpha rece HA tag. Synthetic Thrombopoletin pro

Perfect score:

Title:

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Run

Sequence:

Scoring table:

Searched:

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Database

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Haemagglutinin; epitope; monoclonal antibody; detection; isolation;
fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human influenza virus haemagglutinin epitope peptide fragment #2.
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                                                     AAY06273
AAW77291
AAR81355
AAR81356
AAW73369
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AAW95558
AAY90725
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AAW85003
AAY86206
AAY96709
AAR76070
                      AAB10433
AAY00874
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AAB69626
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AAW08425
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AAY32764
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AAY32768
AAW17789
AAW44013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW59451 standard; peptide; 14 AA
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96DE-1043314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human parainfluenza virus.
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           Modified-site
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Emrich T,
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 RESULT
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pTAT-HA linker enc
Flu-epitope scramb
Flu epitope tagged
Transdominant effe
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Peptide encoded by
Peptide E16853Al f
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19.548 Million cell updates/sec
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                                                                                                                                                                                                                          522463
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                  522463 seqs, 74073290 residues
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                                                        OM protein - protein search, using sw model
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AAY27158
AAB23963
AAB29443
AAW41032
AAW49116
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AAG63605
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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93.8
88.8
85.0
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Score

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Result

Compact Structure
Construct PGGNN-ZE
Exol6 partial prot
Amino acid sequenc
LexA-GAL4 fusion p
HA-tagged I-kappaYeast MSH1 protein

Thrombopoletin pro Epitope tagged TBP Neural cell adhesi

GAL4/HA/NuMA fusio HA1 epitope Infl Mus musculus haema

pSMTN3 fragment fo Peptide encooded b Plasma membrane ta

Influenza haemagg

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AAB07730 standard; Peptide; 34
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                   4 ypydvpdyagsgs 16
    1 YPYDVPDYAGSGS 13
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                                                                      This peptide fragment represents a human influenza virus haemagglutinin eptitope which is used to make monoclonal antibodies with an affinity constant of 108 M-1. Such antibodies are used for detecting and isolating native human influenza virus heemagglutinin (HA), modified HA or HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a chimeric fusion protein of the invention. The specification describes a chimeric pIX protein having at least one adenoviral pIX domain and a non-native amino acid sequence. The non-native sequence is a ligand that binds to a substrate present on surface cells. The chimeric proteins are used for producing adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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Monoclonal antibodies to influenza virus haemagglutinin - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric pIX protein useful in an adenovirus gene transfer vector infecting cells comprises at least one adenoviral pIX domain and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of N-terminal fusion protein of pIX protein.
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                                                                                                                                                                                                          Length 14;
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                                                                                                                                                                                                       DB 19;
2.7e-06;
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Pred. No. 0.00022;
               detecting and isolating haemagglutinin proteins
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100.0%; Pred. No. v..
0; Mismatches
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100.0%; Pred. No. 2.7
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 AAG63605 standard; Protein; 165 AA.
                                         Claim 7; Page 2; 6pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-2001; 2001WO-US04233.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                fusion proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                              AAG63605;
                                                                                                                                                                                                                                                                                                                                                     AAG63605
                                                                                                                                                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a method for isolating one or more genetic elements encoding a gene product with a desired activity. Expression of the genetic element results, directly or indirectly in the modification of an optical property of the encoded polypeptide. The method comprises compartmentalizing the genetic elements into microcapsules, expressing them to produce their respective gene products within the microcapsules, and sorting genetic elements which produce the gene product(s) with the desired activity. The method is used for isolating genetic elements which encode a gene product with a desired activity. This can be a catalytic, regulatory or binding activity. The present sequence represents a fusion of a flag epitope and influenza haemagglutinin. It was used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation of genetic elements encoding a gene product with a desired activity is carried out in microcapsules where changes in optical activity are detected \dot{\,}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Peptide encoded by amplification product encoding a FLAG-HA peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                         Genetic element; optical property; gene product; microcapsule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71; DB 21; Length 34;
Pred. No. 0.00018;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12; Page 79-80; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96992 standard; peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                         06-JAN-2000; 2000WO-GB00030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.8%;
ilarity 92.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tawfik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-465978/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YPYDVPDYAGSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 ypydvpdyagggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA59266.
                                                                                                                                                                         WO200040712-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffiths A,
                                                                                                                                                                                                                                                                                                                                               07-JAN-1999;
                                                                                                                                                                                                                                  13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96992;
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Gaps

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Local Similarity nes 13; Conserv

Query Match Best Local Si Matches 13,

Length 165;

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Synthetic.

(JUEP/)

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The present sequence is the Saccharomyces cerevisiae alpha mating factor receptor Ste2, which was used in the development of a method to prepare cells presenting on their surface a mutant G-protein coupled receptor (GPCR) binding a desired ligand which the natural receptor cannot. The method comprises generating replicable expression plasmids comprising a coding sequence for a GPCR mutated by one or more amino acids in its transmembrane and/or extracellular domains, and operatively linked expression control sequences, transforming host cells with the plasmids and contacting the cells with the plasmids and contacting the cells with the higand and isolating those which bind. GPCR are natural receptor proteins, i.e. membrane proteins that allow cells presenting mutant GPCR on their surfaces are useful as biosensors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with potential applications in diagnostics and environmental and on-line process monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric protein; fusion protein; FLICE like inhibitor protein; FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte; tumour specific antigen; immune response; therapy, prophylaxis; diagnosis; HIV; human immunodeficiency syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cells for surface expression of mutants of natural G\text{-}\mathbf{protein} receptor - where the mutants can bind a ligand that the natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.8%; Score 67; DB 18; Length 481; 92.3%; Pred. No. 0.012; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor cannot, useful as biosensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                       (BRBI-) BRITISH BIOTECH PHARM LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB03963 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus.
                                                                                                                                                                                        97WO-GB00746
                                                                                                                                                                                                                                       96GB-0006126
on-line process monitoring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prar-HA linker polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                               Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.8
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YPYDVPDYAGSGS 13
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-489648/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT85308.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2001
                                                                                          WO9735985-A1
                                                                                                                                                                                        19-MAR-1997;
                                                                                                                                                                                                                                       22-MAR-1996;
                                                                                                                                          02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                       Edwards RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA51738-44 were used to construct a chimeric rat PTH-1 receptor,
rether1 and control plasmids.
Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or
compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or
compounds of the structure or formula signaling functional domain
of parathyroid hormone (PTH); L is a linker molecule present n times
(where n is a positive integer 1-10 (preferably 4); B is a C-terminal
inding portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34);
R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
receptor sequence. The new compounds are used for treating mammalian
conditions characterized by decreases in bone mass, determining rates of
bone reformation, bone resorption and/or bone remodeling, treating
diseases and disorders associated with decreased tetherl activity,
increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
for a peptide or non-peptide PTH (claimed). The new compound can be
administered by inhalation unlike the large native PTH or PTHrP which
avoids the need for regular injections to treat osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linked to a carboxy-terminal binding portion of parathyroid hormone for treating mammallan conditions characterized by decreases in bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compound comprising an amino terminal signaling functional domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                 PTH: parathyroid hormone; conjugate; bone mass; bone reformation; PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
                 Peptide E16853A1 for construction of rTether1 containing HA-tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68; DB 21; Length 32;
Pred. No. 0.00049;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW27158 standard; Protein; 481 AA.
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78.6%;
                                                                                                                                                                                                                                                                                  99WO-US31108.
                                                                                                                                                                                                                                                                                                                                  98US-0114577.
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Best Local Similarity 78.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                             ) GARDELLA T J.
) KRONENBERG H M.
) POTTS J T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YPYDVPDYAGSGSK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-452384/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JUEPPNER H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA51743
                                                                                                                                                                                  WO200039278-A2.
                                                                                                                                                                                                                                                                                  30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                  31-DEC-1998;
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AAW27158;

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AAW27158 RESULT

Sequence

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Lou Gehring's disease; viral infection; HIV; bacterial infection.
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ID AAW4
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                                                                                                                                                                                                                                                                                                                                                                                                              anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in combination with a transport group is described. The transport group is capable of transport group is described. The transport group or fusion peptide across the cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor protein (FLIP) which inhibits Fas and TWF mediated apoptosis by inhibiting binding of Caspase 8 to the Fas receptor complex, thus shutting off the downstream Fas signalling pathway. The chimeric group and fusion peptide are useful for inhibiting ligand-induced apoptosis by bringing them into contact with T cells. The chimeric group is useful for expanding T cells in vitro e.g. T cells specific for particular antigens such as tumour-specific antigen, for enhancing particular antigens such as tumour-specific antigen, for enhancing particular antigens such as tumour-specific antigen, for enhancing are useful for the apoptosis of chronically activated CD4<sup>+</sup> T cells in HIV infected pathents. The chimeric group is also useful for therapeutic, prophylactic or diagnosis of intracellular delivery of small molecules and conding such pash as anti-apoptotic polypeptides and nucleic acids encoding such as anti-apoptotic polypeptides and nucleic cused to amplify the FILP CDNA for subcloning into the XhoI-NcoI site of the pHA-TAT vector which contains the N-terminal protein contains the nucleic access the subclosure and such as an approximant and such as an access to the pHA-TAT vector which contains the N-terminal protein access to the phase of the phase o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein transduction domain; fusion molecule; therapeutic agent; drug targetting; drug discovery; cell transduction; bioavailability; vaccine; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy; seizure; compulsive behaviour; meningitis; encephalitis; ischaemia; spongiform encephalopathy; dyslexia; age-related memory loss;
                                                                                                                                                                                                                                                                                                       Fusion polypeptide useful for inhibiting ligand-induced apoptosis, comprises portion of anti-apoptotic polypeptide linked to a transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein. Tat is a preferred transport moiety.
                                                                                                                                 (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB29443 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 9; 89pp; English.
                                                                                                                                                                                                             Paya C, Algeciras-schminich A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pTAT-HA linker-encoded peptide.
                                                                                                                                                                         (ALGE/) ALGECIRAS-SCHMINICH A.
                                                                                           99US-0128021.
                                   05-APR-2000; 2000WO-US09002.
                                                                           99US-0127867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                               WPI; 2000-664988/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 AA;
                                                                                                                                                                                                                                                                     N-PSDB; AAA54300
                                                                         05-APR-1999;
                                                                                           06-APR-1999;
12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-2001
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The invention relates to a novel fusion molecule comprising at least one protein transduction domain (PTD) and at least one linked molecule, where the linked molecule has therapeutic or prophylactic activity against a medical condition. The invention also relates to methods of drug discovery in which the test compound is linked to a suitable comprising protein and introduced to a cell; a method of killing resistant microorganisms using a suitable fusion molecule, a mammal comprising a covalently linked fusion molecule; and a mammal adapted for experimental use in which at least one transduction molecule has been transduced into essentially all the cells of the mammal. The fusion molecule is used to deliver a therapeutic agent to a mammal, the fusion molecule is used to deliver a therapeutic agent to a mammal. The fusion and exactiovascular frug, an antitumour drug, an anti-infective drug, a cardiovascular frug, an antitumour drug, cardiovascular drug, specially significant or prevention of a central or peripheral nervous system disorder. The central nervous system (CNS) disorder is especially Alsheimer's disease, Parkinson's disease, Huntington's disease, and also includes pre-senile dementia, epilepsy and selzures, computative behaviour, meningitis chementia, epilepsy and selzures, computative behaviour, meningitis cared to kill virally infected cells, especially those infected with HIV. The menory loss or Lou Gehring's disease, Pusion molecules can also be used to kill virally infected related prevent bacterial or viral infections. The methods are a highly effective means for transducing a molecule or systems within it. They also overcome bioavailability problems that a secondard with many theorems with many theorems beloavelled in the method or an analyse or system described with the secondard with many theorems with the delate of the secondard with many theorems with the delate of the secondard with the secondard with the second
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are associated with many therapeutic agents (e.g., large molecular si
hydrophobicity, hydrophilicity, biological resistance), by providing
efficient transduction of the transfer cell. The present sequence
represents a protein transduction domain used in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion molecules comprising protein transduction domains and therapeutic agents, useful for treating e.g. Alzheimer's and Parkinson's diseases, dementia and epilepsy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.2%; Score 65; DB 21; Length 16; 100.0%; Pred. No. 0.00071; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2; 191pp; English.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0122757.
99US-0151291.
                                                                                                                                                                                                                                                                                                                                   28-FEB-2000; 2000WO-US05097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-647439/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YPYDVPDYAGS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAC63859
                                                                                                                                           WO200062067-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-1999;
29-AUG-1999;
                                                                                                                                                                                                                                          19-OCT-2000
                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dowdy SF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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This peptide comprises a Flu epitope tagged scrambled peptide.

Murine 1071/2 Clone 8 cells were infected with pBabe puro

Fetrovirus constructs containing a sequence coding for the Flu

scrambled epitope or an inhibitor peptide (see AAW2917) identical

cother of region of protein Kinase C (PKA) isozymes. Control clone

cother of showed predominantly cytoplasmic and perinuclear staining,

while PMA induced cells showed translocation to the nucleus. Cells

infected with constructs coding for the scrambled peptide showed

similar staining. Those infected with constructs coding for

the C2 region showed predominantly cytoplasmic and perinuclear staining in both control and PMA induced cells. Novel outcomes can

cerening in both control and PMA induced cells. Novel outcomes can

cocur upon expression of peptides in cells. A claimed method of

screening for transdominant intracellular bloactive agents (A) able

co alter the phenotype of a cell comprises: (a) introducing a

library of different randomised nucleic acids (I) into cells; and

(B) screening the cells for altered phenotype due to presence of

(A). Also new are: (I) a library of retroviruses containing

different randomised (I); and (2) a library of mammalian cells

containing the library of (1), preferably integrated into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intracellular transdominant bioactive agent; screening; cell phenotype; effector peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for transdominant intracellular active agents able to alter cell phenotype - useful for examining for changed phenotype, particularly to identify potential drugs with e. g. antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transdominant effector peptide associated screening peptide #49
altered phenotype; retrovirus; library; signal transduction; antitumour; pBABE; influenza virus; flu; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.2%; Score 65; DB 18; Length 1, 100.0%; Pred. No. 0.00076; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 53; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB45969 standard; Peptide; 17 AA.
                                                                                                                                                                                              97WO-US01019
                                                                                                                                                                                                                                          96US-0589911.
96US-0589109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                          (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-393611/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-2001
                                                                                                           WO9727212-A1
                                                                                                                                                                                              23-JAN-1997;
                                                                                                                                                                                                                                       23-JAN-1996;
23-JAN-1996;
                                                                                                                                                     31-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB45969;
                                                                                                                                                                                                                                                                                                                                                      Noaln GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB45969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a scrambled flu-epitope peptide, and can be used in the method of the invention. The method is for screening for transdominant bloactive agents (A) able to alter the phenotype of a comprises: (a) introducing a library of different randomised nucleic acids (I) into cells; and (b) screening the cells for altered phenotype due to presence of (A). (A) are potential pharmaceuticals, from their effect on signalling pathways. A particular application is to identify peptides, encoded by (I), that have antitumour activity or are able to increase sensitivity to, or reduce toxicity of, known antitumour agents. More generally the method can identify agents for treatment of many other conditions, e.g. cardiovascular diseases, anglogenesis, atherosclerosis, obesity, neurodegeneration, bone disease, viral and other infections,
                                                                                                                                                Transdominant bloactive agent; phenotype alteration; signalling pathway; antitumour agent; cardiovascular disease; angiogenesis; atherosclerosis; obesity; neurodegeneration; bone disease; infection; allergy; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for trans-dominant active agents able to alter cell phenotype - useful to identify potential drugs with e. g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transdominant intracellular effector peptide; RNA; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.2%; Score 65; DB 18; L
100.0%; Pred. No. 0.00076;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flu epitope tagged scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 53; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW29116 standard; Peptide; 17
                                                                                                       Flu-epitope scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US01048
                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0589911
96US-0589109
                                                                12-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noaln GP, Rothenberg SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-tumour activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-393612/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YPYDVPDYAGS 11
                                                                                                                                                                                                                       flu-epitope peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                     Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-1997;
                                                                                                                                                                                                                                                                                                                               WO9727213-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-1996;
23-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                          31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergy etc
                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW29116;
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                      AAW41032;
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Wickham TJ;
                                                                                                                                                                          Disclosure; Page 39; 98pp; English.
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                                                                                                                                            therapy of cellular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0634060.
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                                                Roelvink PW,
                                                                             WPI; 1998-169180/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YPYDVPDYAGS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 ypydvpdyags 24
                (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW46332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel in vitro screening methods (I) for a transdominant intracellular bioactive agent capable of altering the phenotype of a cell. (I) comprises: (a) introducing a molecular library of randomized candidate nucleic acids into several cells; and (b) screening the cells for a cell exhibiting an altered phenotype, where the altered phenotype is due to the presence of a transdominant bloactive agent. The methods are particularly useful for screening intracellular transdominant effector peptides and RNA molecules selected inside living cells from randomized pools. (I) is also useful for introducing random libraries into cells to screen for bloactive compounds. The methods allow capid and highly efficient screening of large numbers of random loligoucleocities and their corresponding expression products in a single step. In addition, the methods allow screening in the absence of significant prior characterization of the cellular defect.
                                                                                                                                                                                                                                                                                    Methods for screening intracellular transdominant effector peptides and RNA molecules comprise delivering random oligonucleotides to cells, which are then screened for an altered phenotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Short-shafted adenoviral fibre; ssAF; penton base; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric adenoviral penton base protein epitope 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.2%; Score 65; DB 22; I
100.0%; Pred. No. 0.00076;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 Example 1; Column 79-80; 57pp; English.
                                                                                                                                                                        (STRD ) UNIV LELAND STANFORD JUNIOR. (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW48631 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bispecific antibody; HIV; cancer.
                                                                                           97us-0789333
                                                                                                                          96US-0589108
96US-0589911
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                                                                                                                                                                                                                       Rothenberg SM, Nolan GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                     WPI; 2001-060084/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 ypydvpdyags 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YPYDVPDYAGS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
Unidentified.
                                                                                            23-JAN-1997;
                                                                                                                          23-JAN-1996;
23-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-1996;
                             US6153380-A.
                                                           28-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW48631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW48631
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The present peptide sequence is incorporated into an adenoviral fiber.

The fiber protein and its penton base are used by the adenovirus to

The fiber protein and its penton base are used by the adenovirus to

infect a cell. The invention claims for a transfer vector which contains

bland and an be modified by incorporating sequences for a ligand to a

cell surface receptor or sequences that allow binding to a bispecific

antibody. Bispecific antibodies raised against the present peptide

cell surface receptor or sequences that allow binding to a bispecific

antibody. Bispecific antibodies raised against the present peptide

collows one end of the antibody molecule to bind to the fiber and the

cother end to bind specifically to a cell surface receptor. Therefore

this method enables targeting of the adenovirus to a desired cell-surface

cother by the introduction of a non-native amino acid sequence either

into the penton base or the fibre knob. The non-native amino acid

sequence can be such that it enables direct or indirect binding, e.g. by

consense of a bispecific or multispecific binding agent, of the adenovirus

to the desired cell-surface receptor. Using the a short shafted

adenovirus to attach to a cell and therefore effect entry into the cell

would reduce the level or efficiency of adenoviral penton base binding to

cell-surface receptor, thereby increasing the specificity of binding

to be useful for expressing therapeutic genes, for treating inherited

diseases such as cystic fibrosis or for inducing cell death in

consense and an end of the consense cons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemagglutinin sequence of a chimeric adenovirus penton base protein.
Short-shafted adenoviral fibre constructs - used for producing products that facilitate entry into target cells, useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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This invention describes a novel method for the selection of monoclonal antibodies (MAb) which comprises (1) fusing B lymphocytes with myeloma cells to produce antibody-producing hybridomas by an antibody-binding are presented at the surface of the hybridomas by an antibody-binding protein (I): and (II) binding the antibody to antigons (Ag). The invention also describes antibody-binding proteins (I) that comprise a combination of the signal peptide of a murine immunoglobulin (Ig) kappa chain or a murine MHC (major histocompatibility complex) Class I k(k) molecule; an antibody-binding site of proteins A, G, L or LG, and the transmembrane domain of PDGFR (platelet-derived growth factor receptor) or CD52. The method is used to select MAb with specificity for particular antigens. MAb can be selected without separate culture of hybridomas, and selection can be made against many antigens in a library, optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression vector; antibody binding protein; monoclonal antibody; Neo-R; B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with
treating disorders characterised by inappropriate cell proliferation or cell death
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                       A haemagglutinin (HA) tag peptide (AAR81452) was expressed as a fusion with amino acids 2-221 of apoptosis-associated protein Bcl-Y (see AAR81451) following PCR amplification (see AAT17378-79) of Bcl-Y CDNA and insertion into a CWV-based pcDNA1/amp vector derivative. The HA-Bcl-Y protein was produced in vitro and in transfected COS7 and NIH3T3 cells.
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                                                                                                                                                                                                                                                                                                                           Score 63; DB 17; Length 15;
Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vector pSEX11G2 protein G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10433 standard; Protein; 228 AA.
                                                                 Example 1; Page 65; 100pp; English.
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                                                                                                                                                                                                                                                                                                                               78.8%;
84.6%;
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                  15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB10433;
                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                  The present sequence represents a haemagglutinin sequence of a chimeric adenovirus penton base protein. The peptide is encoded by overlapping oligonucleotides. The penton base protein binds to cell surface receptors called integrins. The integrins not only provide a binding site for the adenovirus penton base protein, but also mediate cellular adhesion to the extracellular matrix molecules. The specification describes a method of introducing an adenovirus into a cell in vitro having a particular cell surface binding site. The adenovirus is contacted with a bispecific molecule comprising a component that selectively binds a binding domain of the penton base protein of the adenovirus and a second component that selectively binds the cell surface binding site. A complex of the adenovirus and the bispecific molecule is formed, and the cell is methods can be used for research and the vectors can be used for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                 Methods for introducing adenovirus into cells - used for genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCl-Y; apoptosis; cell proliferation; cell death; diagnosis; gene therapy; haemagglutinin; HA tag.
                                                                     Roelvink PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.2%; Score 65; DB 19; Length 25; 100.0%; Pred. No. 0.0011; 1ve 0; Mismatches 0; Indels
                                                                     Kovesdi I, McVey DL,
                                                                                                                                                                                                                                                              Example 13; Column 34; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR81452 standard; Peptide; 15 AA.
                                                                                                                                                                                                                        engineering and gene therapy
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                                                                   Bruder JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMUNOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-139648/14.
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N-PSDB; AAV04953-54.
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                           (GENV-) GENVEC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AA;
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09-AUG-1994;
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                                                                 Brough DE,
Wickham TJ;
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on the basis of strength of affinity for a particular antigen. Complex mixtures of hybridomas can be used for selection, reducing the time and cost involved in MAD selection. This sequence represents the protein G contained in the expression vector pSEX11G2 which contains the protein G, Neo-R and the bla protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a vaccine comprising a cell having a membrane-bound fusion protein (FP) consisting of a non-antibody immunomodulator (I) linked to a heterologous membrane attachment domain. The vaccines are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GM-CSF; granulocyte macrophage colony stimulating factor; vaccine; membrane-bound fusion protein; non-antibody immunomodulator; infection; membrane attachment domain; cancer; autoimmune disease; therapy.
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine having a membrane-bound fusion protein - comprising an Immunomodulator and heterologous membrane attachment domain useful for modulation of immune response against a disease-associated
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0
                                                                                                                                                        Score 62; DB 21; Length 228; Pred. No. 0.034;
                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the pHOOK-1.GM-CSF fusion protein. The
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                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOOK-1.GM-CSF fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
220
                                                                                                                                                                                                                                                                                                                                                AAY00874 standard; Protein; 232 AA
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                                                                                                                                                                                           1;
                                                                                                                                                          77.5%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                           10; Conservative
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Chimeric - Synthetic.
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                                                                                                                                                                                                                                                1 YPYDVPDYAGS 11
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                          228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX27068
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                                                                                                                                                                                                                                                                                                                                                                                AAY 00874;
                                                                                                          Sequence
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for treatment or prevention of the appropriate tumour type, e.g. based on histological analysis. Membrane-bound (1) provides a vaccine with increased receptor-cytokine avidity, and thus stimulates a stronger
                                                                                                                                                                    Gaps
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                                                                                                                              Score 62; DB 20; Length 232;
Pred. No. 0.035;
1; Mismatches 0; Indels
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                                                                                                                                77.5%;
90.9%;
                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 10; Conserv
                                                                                   232 AA;
                                                                                     Sequence
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Sequence 51, Application US/08789338F

Patent No. 6153380

GENERAL INFORMATION:
APPLICANT: No. 6153380an, Garry P
APPLICANT: Rothenberg, S. M.
TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
FILE REFRENCE: A642601DJBRASSS
CURRENT APPLICATION NUMBER: US/08/789, 333F
CURRENT FILING DATE: 1997-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.0
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Appli
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; Sequence 15, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
    APPLICANT DOWGL
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/09/208,966
; CURRENT FILING DATE: 1998-1-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER APPLICATION NUMBER: 60/069,012
; EARLIER PILING DATE: 1998-04-20
; EARLIER PILING DATE: 1997-12-10
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 15; LENGTH: 16
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US-08-470-837-28
US-08-478-386A-19
US-08-6292-597-19
US-08-622-267A-60
US-08-922-267A-60
US-08-90-011A-17
US-08-690-011A-49
US-08-685-625A-4
US-08-687-559-14
US-08-687-559-14
US-08-687-559-14
US-08-687-559-14
US-08-887-5378-3
US-08-887-5378-3
US-08-887-7378-19
US-08-887-738-19
US-08-887-738-19
US-08-887-738-19
US-08-887-738-19
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US-08-887-738-19
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100.0%; Pred. No. 0.00.
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Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: human
US-09-208-966-15
         RESULT 2
US-08-789-333F-51
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Sequence 51,
Sequence 27,
Sequence 10,
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:: \cqqn2_6\ptodata/2/laa/5A_COMB.pep:*

:: \cqn2_6\ptodata/2/laa/5B_COMB.pep:*

:: \cqn2_6\ptodata/2/laa/6A_COMB.pep:*

:: \cqn2_6\ptodata/2/laa/6B_COMB.pep:*

:: \cqn2_6\ptodata/2/laa/PCTUS_COMB.pep:*

:: \cqn2_6\ptodata/2/laa/PCTUS_COMB.pep:*

:: \cqn2_6\ptodata/2/laa/PCTUS_COMB.pep:*

:: \cqn2_6\ptodata/2/laa/PCTUS_COMB.pep:*
                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-208-966-15
US-08-704-060-27
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US-08-321-071A-5
US-08-992-151-2
US-08-992-151-2
US-08-992-951-2
US-08-992-951-6
US-08-992-951-6
US-08-992-951-6
US-08-992-951-6
US-08-992-951-6
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US-08-992-913-39
US-08-992-913-39
US-08-992-913-7
US-08-991-913-98
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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No.
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APPLICANT: CHITTENDEN, Thomas D.
TITLE OF INVENTION: APOPTOSIS RELATED PROTEIN BC1-Y, AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: Z0004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                   Sequence 10, Application US/08700846
Patent No. 5962311
GENERAL INFORMATION:
PETRUS W.
APPLICANT: WICKHAW, THOMAS J.
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSE:
ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 2; L
Pred. No. 0.00055;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/700,846 FILING DATE: 21-AUG-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08321071A Patent No. 5672686 GENERAL INFORMATION:
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NAME: LARCHER, CAROL
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPAX: (312) 616-5600
TELEPAX: (312) 616-5700
INFORMATION FOR SEQ 1D NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
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    14 YPYDVPDYAGS 24
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STREET: TWO PRU
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                RESULT 4
US-08-700-846-10
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US-08-321-071A-5
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APPLICANT: Wovesdi, Imre
APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: THE ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY
TITLE OF INVENTION: THE ADENOVIRAL-MEDIATED RASE PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                         Gaps
                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: epitope tag
OTHER INFORMATION: sequence.
US-08-789-333F-51
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                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
                                                                                                                                                                                                           Score 65; DB 4; Le
Pred. No. 0.00037;
0; Mismatches 0;
                                                                                                                                                                                            81.2%; SCUL.
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: K117k, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 711
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids
                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                       Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.2
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Chicago
STATE: Illinois
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SEQ ID NO 51
LENGTH: 17
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APPLICANT: YANG, ZHI
TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY
TITLE OF INVENTION: DEPOTED TITLE OF INVENTION: DEPOTED TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: MOTTION & FOOTSTER
                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08990140A

Sequence 13, Application US/08990140A

Patent No. 6093795

GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
APPLICANT: Sonenberg, Nahum
APPLICANT: Sonenberg, Nahum
TITLE OF INVENTION: Human Prt1-11ke Subunit Protein (hPrt1) and Human
TITLE OF INVENTION: elf4GF-11ke Protein (p97) Genes
FILE REFERENCE: 1488.0700001
CURRENT APPLICATION NUMBER: US/08/990,140A

CURRENT APPLICATION NUMBER: US 60/033,151
EARLIER FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

LENGTH: 10

LENGTH: 10

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                                                                                                                                                               Length 219;
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Pred. No. 0.00088;
                                                                                                                                                                                                          0; Indels
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                                                                                                                                                             Score 62; DB 2;
Pred. No. 0.016;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.2%; Scc. 100.0%; Pred. No. v. 0. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08282951
Patent No. 5665590
                                                                                                                                                               77.5%;
90.9%;
  SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                  Query Match 77.5
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                              , MOLECULE TYPE: protein US-08-902-516-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRCANISM: Homo saplens
US-08-990-140-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   1 YPYDVPDYAGS 11
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22 YPYDVPDYAGA 32
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US-08-282-951-2
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COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME
50
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                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,071A
FILING DATE: US/08/321,071A
FILING DATE: US/08/321,071A
FILING DATE: US/08/321,071A
PRIOR APPLICATION S14
PRIOR APPLICATION NUMBER: US/08/321,0103
FILING DATE: 09-AUG-1995
PROR APPLICATION NUMBER: 09-8UG-1995
ATFORMEY/AGENT INPORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REGISTRATION NUMBER: 32,073
REGISTRATION NUMBER: 32,073
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 32,073
RELECOMMUNICATION S10-942-8400
TELEFAK: 202-942-8409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: (211fornia
COUNTRY: United States
LDF: 92121
COMPUTER RELABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL.1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGIGSRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELERAX: (619)535-909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08902516
Patent No. 5891432
GENERAL INFORMATION:
APPLICANT: SOO HOO, William
TITLE OF INVENTION: COMPRISING GM-
TITLE OF INVENTION: RESPONSE USING
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.8%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.8
Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YPYDVPDYASLGS 15
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Gaps

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Sequence 1, Application US/08723726

Patent No. 5851521

GENERAL INFORMATION:
APPLICANT: BRANELLEC, Didier
APPLICANT: ISNER, Jeffrey M.
APPLICANT: ISNER, Jeffrey M.
APPLICANT: BENEFLE, Patrice
TITLE OF INVENTION: WIRAL VECTORS AND THEIR USE FOR TREATING
TITLE OF INVENTION: HYPERPROLIFERATIVE DISORDERS, IN PARTICULAR RESTENOSIS
NUMBER OF SEQUENCES. 3
CORRESPONDENCE ADDRESS:
                                                                 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                  Score 60.5; DB 1; Length 272;
Pred. No. 0.035;
1; Mismatches 0; Indels
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Pred. No. 0.0026;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,726
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PURDR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/04493
FILING DATE: 28-MAR-1996
FILING DATE: 38-MAR-1996
ATORNEY/AGENT INCORMATION:
REFERENCE/DOCKET NUMBER: ER 95-04234
ATORNEY/AGENT INCORMATION:
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95022A-US
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHANGE: (610)454-3816
TELECHANGE: (610)454-3816
                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: Mail Drop 3C43, P.O. Box 5093
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: PA
COUNTRY: USA
ZIP: 19426-0997
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                    75.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.8%;
                  Query Match 75.6
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                     227 YPYDVPDYAPNKGSGT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 14' amino acids
                                                                                                        1 YPYDVPDYA---GSGS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YPYDVPDYASLG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-390-874C-13
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US-08-723-726-1
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Patent No. 5665590
GENERAL INFORMATION:
APPLICANT: YANG, ZHI
TITLE OF INVENTION: METHOD FOR ISOLATING AND DIRECTLY
TITLE OF INVENTION: CLONING GENES WHICH ENCODE CELL-SURFACE AND SECRETED
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60.5; DB 1; Length 102;
Pred. No. 0.012;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,951
FILING DATE: 29-JUL-1994
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33 943
REFERENCE/DOCKET NUMBER: 20296-20012.00
TELECOMMUNICATION INFORMATION:
TELEPRAN: (415) 813-560
TELERAX: (415) 494-0792
TELERAX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       20296-20012.00
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,951
FILING DATE: 29-UUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/POCKET NUMBER: 2029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELERA: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                           : 102 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 272 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.6
Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YPYDVPDYA---GSGS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-282-951-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-282-951-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                        linear
                                                             FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Gaps

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Sequence 52, Application US/09169015
Patent No. 6180343
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
FILE REFERENCE: A6600/Dab/RmS/SJR
CURRENT FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-169-015-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.8%; Score 59; DB 4; Length 19;
83.3%; Pred. No. 0.0035;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 4; Length 16;
Pred. No. 0.0029;
0; Mismatches 2; Indels
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Patent No. 6306649
GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
                           FILING DATE: 10-MAR-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,874
FILING DATE: 17-FEB-1995
ATTORNEY-AGENT INFORMATION:
NAME: DOW, Karen B.
REGISTRATION NUMBER: 29,684
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 02307K-057010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
UMBER: US/09/265,772
10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: peptide US-09-265-772-13
            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YPYDVPDYAGSG 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-672-213-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-169-015-52
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                                                                               PAPLICANT: Milliams, Lewis T.

APPLICANT: Milliams, Lewis T.

TITLE OF INVENTION: A Constitutively Active
TITLE OF INVENTION: Phosphatidylinositol 3-Kinase and Uses Thereof
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: Two Embarcadero Center, Eighth Floor
STATE: Two Embarcadero Center, Eighth Floor
COUNTR: USA
ZIP: 94111-3834
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDB PC compatible
COMPUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: A Constitutively Active
TITLE OF INVENTION: Phosphatidylinositol 3-Kinase and Uses Thereof
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 0.0029;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
      Sequence 13, Application US/08390874C Patent No. 6043062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09265772 Patent No. 6300111 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 16 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.8
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YPYDVPDYAGSG 12
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TOPOLOGY: 1
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Gaps

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73.8%; Score 59; DB 4; Length 40; 83.3%; Pred. No. 0.0078; tive 0; Mismatches 2; Indels
                PELICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
FILING DATE: 27-JUN-1995
PRICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY,FAGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 346B
TELECOMUNICATION INFORMATION:
TELEPANCE: 617-494-0400
TELEPAK: 617-494-0400
TELEPAK: 617-494-0400
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
LENGTH: 40 amino acids
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Best Local Similarity 83.3'
Matches 10; Conservative
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MOLECULE TYPE: protein US-08-672-213-29
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Fatent No. 6306649
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Gene Therapeutics, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 4; Leuy...
Pred. No. 0.0051;
----hes 2; Indels
                                                                                                                                              COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN 1996
CLASSIFICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION NUMBER: US 60/019,614
FILING DATE: 27-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, DAVIG L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 346B
TELECOMMUNICATION INFORMATION:
TELEPRAN: 617-494-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTR: USA
ZIP: 02139-4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                       E: ARIAD Gene Therapeutics, Inc.26 Landsdowne Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.83
Best Local Similarity 83.33
Matches 10; Conservative
                                                             CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-672-213-39
CORRESPONDENCE ADDRESS:
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02139-4234
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0; Gaps

30 55 68.8 550 1 HMIV98 hemagglutinin prec 31 55 68.8 550 1 HMIV15 hemagglutinin prec 32 55 68.8 550 1 HMIV86 hemagglutinin prec 33 55 68.8 550 2 JOI153 hemagglutinin prec	4 55 68.8 550 2 J01154 hemagglutinin 5 55 68.8 550 2 J01155 hemagglutinin	55 68.8 565 1 HMIVE hemagglutinin hemagglutinin 55 68.8 565 1 HMIVE hemagglutinin hemagglutinin 55 68.8 566 1 HMIVE hemagglutinin hemagglutinin hemagglutinin hemagglutinin hemagglutinin hemagglutinin	1 55 68.8 566 1 HMIVY hm hemagglutinin	4 34 67.5 565 1 HMIVES indimaystucinii 5 54 67.5 565 1 HMIVES	ALIGNMENTS		RESULT 1 JU2374 hemagglutinin - influenza A virus (strain SN1289)	C;Species: intudenza A virus C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999 C;Accession: JQ2374 R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.	J. Gen. Virol. 74, 2313-7218, 1993 A;Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtain A;Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtain A;Teference number: JQ2369; MUID:94065682 A;Accession: JQ2374 A;MOlecule type: mRNA A;Residues: 1-330 <rqc></rqc>	A;Cross-references: GB:LZQ115 A;Experimental source: subtype H3N2 C;Superfamily: influenza virus hemagglutinin	Query Match 68.8%; Score 55; DB 2; Length 330; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	O. 1 VDVINUDIVA G	98 YPYDVPDYA		;		R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J. J. Gen. Virol. 74, 2513-2518, 1993	A;Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtain A;Reference number: JQ2369; MUID:94065682	A; Accession: JQ2375 A: Molecule type: mRNA	A; Residues: 1.330 cROC> A; Cross-references: GB:L20119	A; Experimental source: subtype H3N2 C; Superfamily: influenza virus hemagglutinin	68,88; Sc	Pred. No. 0.14 0; Mismatches	Qy 1 YPYDVPDYA 9
4.5 Compugen Ltd.		arch time 27.06 Seconds (without alignments) 39.410 Million cell updates/sec				rs: 219241				cted by chance to have a of the result being printed, score distribution.		Description	hemagglutinin - in hemagglutinin - in hemagglutinin - in	1	·								pre	hemagglutinin prec hemagglutinin prec hemagglutinin prec hemagalutinin prec
GenCore version 4.5 Copyright (c) 1993 - 2000 Com	OM protein - protein search, using sw model	, 10:16:16 ; Se	Title: US-09-284-787-2 Perfect score: 80 Sequence: 1 YPYDVPDYAGSGSK 14	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 219241 seqs, 76174552 residues	Total number of hits satisfying chosen parameters	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : PIR_68:* 1: plr1:* 2: plr2:* 3: plr3:* 4: plr4:*	Pred. No. is the number of results predicted score greater than or equal to the score of t and is derived by analysis of the total score	Query	Score	1 55 68.8 330 2 JO2374 2 55 68.8 330 2 JO2375 3 55 68.8 331 2 JO2377 4 55 68 331 2 JO2377	55 68.8 347 2 55 68.8 347 2	55 68.8 347 2 55 68.8 347 2	55 68.8 347 2 55 68.8 347 2	55 68.8 347 2 55 68.8 347 2	55 68.8 347 2 55 68.8 347 2	55 68.8 347 2 55 68.8 362 2	55 68,8 550 1 55 68.8 550 1 55 68.8 550 1	55 68.8 550 1 55 68.8 550 1 55 68.8 550 1			

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A; Molecule type: mRNA
A; Residues: 1-134, K',136-156, L',158-173, F',175-188, S',190-218, F',220-225, L',227
A; Cross-references: EMBL:246395; NID:g609027; PIDN:CAA86530.1; PID:g1228087
A; Rogerimental source: isolate A/England/269/93
A; Accession: S52181
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A; Residues: 1-74, N', 76-120, 'T', 122-156,'L', 158-173,'F',175-188,'S',190-200,'K',202-2
A; Cross-references: EMBL:246402; NID:9609041; PIDN:CAA86537.1; PID:9609042
A; Experimental source: isolate A/England/471/93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-74, 'N', 76-120, 'T', 122-156, 'L', 158-173, 'F', 175-188,'S', 190-200,'K', 202-2
A; Residues: EMBL:246413; NID: 9609059; PIDN: CAA86548.1; PID: 9609060
A; Experimental source: isolate A/Scotland/142/93
C; Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-134, K,/136-156, L',158-173, F',175-188, S',190-218, F',220-225, L',227
A;Cross-references: EMBL:246399; NID:9609035; PIDN:CAA86534.1; PID:9609036
A;Experimental source: isolate A/England/328/93
A;Experimental source: 552194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-134, K',136-156, L',158-173, F',175-188, S',190-218, F',220-225, L',227
A;Crosz-references: EMBL:246415; NID:9609065; PIDN:CAA86550.1; PID:9609066
A;Experimental source: isolate A/Scotland/174/93
A;Accession: S52184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-134,'K',136-156,'L',158-173,'F',175-188,'S',190-218,'F',220-225,'L',227
A;Cross-references: EMBL:246414; NID:9609061; PIDN:CAA86549.1; PID:9609062
A;Experimental source: isolate A/Scotland/160/93
A;Accession: S52196
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A;Variety: isolate A/Beijing/353/89
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
                                                                                                                    A;Molecule type: mRNA
*Residues: 1-347 CEL3-
A;Gross-references: EMBL:Z46409; NID:9609057; PIDN:CAA86544.1; PID:9609058
A;Experimental_source: isolate A/Hong Kong/34/90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-347 <ELL>
A; Cross-references: EMBL:246391; NID:g609022; PIDN:CAA86526.1; PID:g609023
A; Experimental source: isolate A/Beijing/353/89
C; Superfamily: influenza virus hemagglutinin
                            A;Cross-references: EMBL:Z46410; NID:g609053; PIDN:CAA86545.1; PID:g609054
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A; Description: Antigenic and genetic variation in the haemagglutinin
A; Reference number: S52173
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100.0%; Pred. No. 0.15;
iive 0; Mismatches
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                                                        A; Experimental source: isolate A/Hong Kong/23/92
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
A; Residues: 1-347 <EL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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                                                                                                                                                                                                                                            A; Accession: S52177
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R; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A; Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained A; Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained A; Reference number: J02369; MUID:94065682
A; Reference number: MRNA
A; Molecule type: mRNA
A; Residues: 1-331 < ROC>
A; Residues: 1-331 < ROC>
A; Residues: subtype H3N2
C; Superimental source: subtype H3N2
C; Superimental: Influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: influenza A virus
C:Species: influenza A virus
C:Species: influenza A virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: J03378
B;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (HIN1 and H3N2) haemagglutinin sequences obtained
A;Reference number: J02378
A;Reference number: J02378
A;Residues: 1-331 <-ROC>
A;Residues: 1-331 <-ROC>
A;Residues: 1-331 cROC>
A;Cross-references: GB:L20102
A;Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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C; Species: influenza A virus
C; Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C; Accession: S52173; S52190; S52192; S52181; S52184; S52196; S52184; S52193
R; Ellis, J.S.
R; Ellis, J.S.
Bubmitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: S52173
A; Accession: S52173
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                                                                                                                                             C;Species: influenza A virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
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A;Residues: 1-347 <ELL.A
A;Cross-references: EMBL:246392; NID:g609020; PIDN:CAA86527.1; PID:g609021
A;Experimental_source: isolate A/Beijing/32/92
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100.0%; Pred. No. v...
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A; Molecule type: mRNA
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Algorithm of the EMBL Data Library, October 1994
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Algorithm Antigenic S2179
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hemagglutinin - influenza A virus (isolate A/England/289/93) (fragment)
c;species: influenza A virus
A virus
A;variety: isolate A/England/289/93
C;bate: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
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A:Variety: isolate A/England/286/93
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
   A;Molecule type: mRNA
A;Residues: 1-347 <ELL>
A;Cross-references: EMBL:246396; NID:g609029; PIDN:CAA86531.1; PID:g609030
A;Experimental source: isolate A/England/284/93
C;Superfamily: influenza virus hemagglutinin
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C.Specides: influenza A virus
C.Specides: influenza A.England/247/93
C.Specides: influenza influenza virus isolate A.England/247/93
C.Specides: influenza virus hemagglutinin of recently circula A.Recession: 552173
A.Recession: 552173
A.Reciperimental sources: EMBL:246394; NID:g609025; PIDN:CAA86529.1; PID:g609026
A.Experimental source: isolate A.England/247/93
C.Superfamily: influenza virus hemagglutinin
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A;Varlety: isolate A/England/284/93
A;Varlety: isolate A/England/284/93
A;Varlety: isolate A/England/284/93
C;Accession: S52178
B;Ellis, J.S.
A;Description: Antigenic. and genetic variation in the haemagglutinin of recently circula A;Reference number: S52173
A;Accession: S52173
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R; Ellis, J.S.
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C;Species: influenza A virus
C;Species: influence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52183
C;Accession: S52183
A;Bellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Bescription: Antigenic and genetic variation in the haemagglutinin of recently circula A;Reference number: S52183
A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: A;Acc
                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circula
A; Reference number: 552173
A; References: 552182
A; Molecule type: mRNA
A; Residues: 1-347 < ELLD.
A; Residues: 1-347 < ELLD.
A; Residues: 1-347 < ELLD.
A; Crooss-references: EMBL:246400; NID:9609037; PIDN:CAA86535.1; PID:9609038
A; Experimental source: 1solate A/England/346/93
C; Superfamily: influenza virus hemagglutinin
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R;Ellis, J.S.
Rstlis, J.S.
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Rstlis, J.S.
Rstlis, J.S.
Ribmitted to the EMBL Data Library, October 1994
Rybescription: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: $52173
Rybescription: Antigenic and genetic variation in the haemagglutinin of recently circula A; Reference number: $52173
Rybescription: A77 < ELL>
Rybescription: R
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C;Species: influenza A virus
A;Variety: isolate A/England/328/93
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession. 352182
Sibmitted to the EMBL Data Library, October 1994
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C;Species: influenza A virus
A;Variety: isolate A/England/67/94
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
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Pred. No. 0.15;
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Matches 9; Conservative
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submitted to the EMBL Data Library, October 1994
A; Description: Antigenic and genetic variation in the haemagglutinin of recently circ
A; Reference number: $52173
A; Accession: $52186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-347 <ELL>.
A; Rosidues: 1-347 <ELL>.
A; Cross-references: EMBL: Z46404; NID:g609045; PIDN:CAA86539.1; PID:g609046
A; Experimental source: isolate A/England/68/94
C; Superfamily: influenza virus hemagglutinin
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100.0%; Pre
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REDLINE=81030852; PubMed=7421990;

RA Gething M.-J., Bye J., Skehel J.J., Waterfield M.;

Gething and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and DNA sequence of double-stranded copies of haemagglutinin RT denses from H2 and H3 strains elucidates antigenic shift and drift in human influenza virus.*;

Nature 287:301-306(1980).

CELL RECEPTORS AND FOR INITIATING INFECTION.

CELL RECEPTORS AND FOR INITIATING INFECTION.

CHAIN AND HA2) LINKED BY A DISGULFIDE BOND.

CI- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

DR PIR; A04051; HM1VH.

DR PIR; A04051; HM37; Hemagglutn.

DR PIR; A04051; Hemagglutn.

DR PEAM: PROBO0225; Hemagglutn.

DR PEAM: PROBO0225; Hemagglutn.

T 1 16

ET GARBOHYD 24 24 N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD 38 38 N-LINKED (GLCNAC. ..) (POTENTIAL).

FT CARBOHYD 97 97 N-LINKED (GLCNAC. ..) (POTENTIAL).
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN]
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                                                                                                                                                                                                                                                                                                                                                 Influenza A virus (strain X-31).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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HEWA_IAHUR
HEWA_IADU3
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HEWA_IAZU4
HEWA_IAZU4
HEWA_IAZU4
HEWA_IAHU6
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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HEMA_IAME1
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                 antigenicity.";
J. Virol. 37:845-853(1981).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: HOMOTRIMER, EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                         MEDLINE-81194918; PubMed-6164798; Sleigh M., Border V.J.; Sleigh M.J., Borh G.W., Underwood P.A., Bender V.J.; Mattigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral
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                                                                                     13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAI CHAIN] (FRAGMENT).
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13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAI CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.8%; Score 55; DB 1; Length 328; 100.0%; Pred. No. 0.069;
                                                                                                                                                                                                 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus,
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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8 N-LINKED (GLCNAC. . .) (POTE
22 N-LINKED (GLCNAC. . .) (POTE
38 N-LINKED (GLCNAC. . .) (POTE
63 N-LINKED (GLCNAC. . .) (POTE
165 N-LINKED (GLCNAC. . .) (POTE
285 N-LINKED (GLCNAC. . .) (POTE
285 N-LINKED (GLCNAC. . .) (POTE
328 N-LINKED (GLCNAC. . .) (POTE
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                     328 AA
                                                                                                                                                                                Influenza A virus (strain A/England/878/69).
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                     PRT;
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last seq
20-AUG-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; K03335; AAA43184.1; -.
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Best Local Similarity 100.
Matches 9; Conservative
                   STANDARD;
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                HEMA_IAEN6
P04664;
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P04663;
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CARBOHYD
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SEQUENCE
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                       ALD DESCRIPTION OF THE PRINT OF
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                                                                                                                                                                                         J. VÍrol. 37:845-853(1981).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPPORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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Both G.W., Sleigh W.J.;

"Conservation and variation in the hemagglutinins of Hong Kong

subtype influenza virtuses during antigenic drift.";

J. Virol. 39:663-672(1981).
                                          SEQUENCE FROM N.A.
MEDIATE-81194918; PubMed-6164798;
Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.;
Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral antigenicity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55; DB 1; Lenyc...
---d. No. 0.069;
0; Indels
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Envelope protein; Hemagglutinin; Glycoprotein.
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MEDLINE=82033259; Pubmed=6169840;
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Pfam; PF00509; Hemagglutinin; 1.
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100.0%;
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Best Local Similarity
Matches 9; Conserv
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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There are no restrictions on it
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-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
           SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND. SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-87265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                GGCNAC. ) (POTENTIAL).
O GGLCNAC. ) (POTENTIAL).
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191582, 084021; 084022; 01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 14), Last annoctation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN); HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.8%; Score 55; DB 1; Length 550; 100.0%; Pred. No. 0.12;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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 CELL RECEPTORS AND FOR INITIATING INFECTION
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HEMAGGLUTININ HA2
                                                                                                                                                                                                 InterPro; IPR001364; Hemagglutn.
Pfam. PF00509; Hemagglutinin; 1.
ProDon; PD000225; Hemagglutin; 1.
NON_TER I Hemagglutinin; Glycoprotein.
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Conservative 0; Mismatches
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Σ
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                                                                                                                                                                                                                                                                                                                                                                                                                61699
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Best Local Similarity
Matches 9; Conserv
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-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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BEDLINE-37265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;

Antigenic and genetic conservation of H3 influenza virus in wild
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P12583; Q84011;
01-0CT-1989 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
NCBI_TaxID=11358;
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Pred. No. 0.12;
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                                                                                                                                                                  PIR; A27813; HM1V//,
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; I.
ProDom; PD000225; Hemagglutni; I.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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Best Local Similarity
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N-LINKED (GLCNAC

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-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
                                                                                                                                                                                                   Gaps
                                             N-LINKED (GLCNAC. . ) (POTENTIAL).
K -> N (IN PIR DATA BANK).
W; A107023ACC9CC353 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-87265458; Pubmed-2440178; Kida H., Kawaoka Y., Naeve C.W., Webster R.G.; "Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                           HEMA_IADH3 STANDARD; PRT; 550 AA.
P12584; Q84012; Q89793;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HA1 CHAIN; HEMAGGLUTININ HA2 CHAIN) (FRAGMENT).
                                                                                                                                                                       // Match 68.8%; Score 55; DB 1; Length 550;
Local Similarity 100.0%; Pred. No. 0.12;
hes 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                         HEMAGGLUTININ HA1 CHAIN.
HEMAGGLUTININ HA2 CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Duck/Hokkaido/33/80).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M16739; AAA43145.1; -.
PIR; C27813; HMXV33.
InterPro; IPR001364; Hemagglutn.
Probom; PD000225; Hemagglutnin; 1.
Probom; PD000225; Hemagglutnin; 1.
Envelope protein; Hemagglutnin; 1.
I 1
CHAIN TER I 1 328
HEMAGGLUTININ HAI
Hemagglutinin; Glycoprotein
                                                                                                                                                                                                 0; Mismatches
                                                                                                                                      61659 MW;
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                                   330
22
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137
550 AA;
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  Envelope protein;
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-!- FUNCTION: HEWAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPORSA BAND FOR INITITATING INFECTION.

-!- SUBUNT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFUGENZA HEMAGGLUTININ FAMILY.
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                             HEMA_IADH4 STANDARD; PRT; 550 AA.
P12585; 084013; 0840114;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
20-AbG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAZ CHAIN) (FRAGMENT).
                                                                                  Length 550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza A virus (strain A/Duck/Hokkaido/7/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
-LINKED (GLCNAC. . .) (F
6C30BF67CFDCB7DE CRC64;
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                                                                              Score 55; DB 1;
Pred. No. 0.12;
; Mismatches 0
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                                                                                  68.8%; Score 55; 100.0%; Pred. No.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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                    61577 MW;
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Best Local Similarity 100..
Post Local 9; Conservative
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                    550 AA;
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Best Local Similarity
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HEMA_IADH4
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PIR; G27813; HMIV15
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                                                                                                                                    NCBI_TaxID=11363;
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P43257;
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HEMA_IADHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              VITOLOGY 159:109-119(1987).

-1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO ECLL RESPERPORS AND FOR INITIATING INFECTION.

-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HAZ CHAIN.
N-LINED (GLCNAC. .) (POTENTIAL).
Y-> N (IN PIR DATA BANK).
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
ducks.";
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                                                                                           HEMA_IADH6 STANDARD; PRT; 550 AA.
12587; 084017;
01-0CT-1899 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECIRSOR (CONPAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 550;
                                                                                                                                                                                                                                               Influenza A virus (strain A/Duck/Hokkaido/9/85).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A Virus.
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0.12;
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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Best Local Similarity
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HEMA_IADH7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 159:109-119(1987).
-!- FUNCTION: HERAGGLOTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL PECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                        MEDLINE-67265458; Pubmed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Viruses; sRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                      Influenza A virus (strain A/Duck/Hokkaido/10/85).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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          Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
"Molbecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.",
J. Gen. Virol. 72:2007-2010(1991).
-i- FUNTION: HEMAGGLUTINN IS RESPONSTBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
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Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS
                                                                                                   -1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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ProDom, PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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MEDLINE-91341491; PubMed-1875195;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
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Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Knog/GB (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991)
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFRECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOWMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND.
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                                  -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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00-NGV-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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AND HA2) LINKED BY A DISULFIDE BOND
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Pfam; PF00509; Hemagglutinin; 1.
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-1- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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Yasuda J., Shortridge K.F., Shintzu Y., Kida H.;
Yasuda J., Shortridge K.F., Shintzu Y., Kida H.;

Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kongy'68 (H3NZ) strain emerged.";

J. Gen. Virol. 72:2007-2010(1991).

-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITATING INFECTION.
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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00.NOG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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ProDom; P0000225; Hemagglutni; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
                              EMBL; D00932; BAA00772.1; -.
InterPro; IPR001364; Hemagglutn.
ProDom; P000025; Hemagglutnin; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 40, Last annotation update)
EQ-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                       Length 550
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
N-LINKED (GLCNAC. ..) (POT)
W: 9A1E094DA28BACD2 CRC64;
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. 0.12;
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                                                                                                                                                                                       Score 55;
Pred. No.
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Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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SQ SEQUENCE 550 AA; 61804 MW; 52C9F14B309310ED CRC64;

0; Gaps Query Match

68.8%; Score 55; DB 1; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels

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Search completed: April 11, 2002, 10:22:00 Job time: 430 sec

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20 22 23 23 23	22 22 22 23 24 25 26 26 27	33333	1 0 0 C	7 8 6 ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° °	4 4 4 4 0 11 0 E	44 45	0.8			RP RA RY			Query M Best Lo Matches	Oy Dp	RESULT 09W8T9 ID 09 AC 09
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model Run on: April 11, 2002, 10:22:57 ; Search time 50.04 Seconds . (without alignments) 40.924 Million cell updates/sec	Title: US-09-284-787-2 Perfect score: 80 Sequence: 1 YPYDVPDYAGSGSK 14	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	473505 segs, 146272329 residues	Total number of hits satisfying chosen parameters: 473505 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : SPTREMBL_17:*  1: SP_archea:* 2: Sp_bacteria:* 3: Sp_fungi:* 4: Sp_fungi:* 5: Sp_fungi:*	5: Sp_inverceblace:* 6: Sp_manmal:* 7: Sp_nho:* 8: Sp_organelle:* 9: Sp_phage:*	10: sp_plant:* 11: sp_rodent:* 12: sp_vrus:* 13: sp_vertebrate:* 14: sp_unclassified:*	of res qual to sis of	SUMMARIES  Result Query  No. Score Match Length DB ID  Description	55 68.8 236.12 Q9W821 Q9w821 influenza 55 68.8 236.12 Q9W879 Q9w8E9 influenza 55 68.8 236.12 Q9W877 Q9w877 Q9w877 Q9w877 influenza 65 68.8 286.12 Q9W126 Q9w126 Q9w126 G0w125 influenza 55 68.8 286.12 Q9W126 G0w126	9 55 68.8 325 12 040779 040779 040779 16fluenza 090779 16	1 55 68.8 327 12 040780 092324 Influenza 2 55 68.8 327 12 092325 092325 10fluenza 3 55 68.8 327 12 092327 092327 10fluenza 4 55 68.8 327 12 092327 092327 10fluenza 4 55 68.8 327 12 097790 094750 10fluenza	55 68.8 327 12 Q9YT89 Q9Yt89 Q9Yt88 15 68.8 327 12 Q9YT87 Q9Yt88 in Q9Yt88 in Q9Yt87 Q9Yt87 Q9Yt87 in Q9Yt87 in Q9Yt87 in Q9Yt87 in Q9Yt86 in Q9Yt89 in Q9Yt

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STRAIN-TOKYO1560, TOKYO1567, TOKYO1569, STRAIN-TOKYO1570, TOKYO1569, Mori S., Sekine H.;
"HAI domain of Influenza A (H3N2) virus.";
Submitted (LAX-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB013813; BAA77287.1;
EMBL; AB013810; BAA77287.1;
EMBL; AB013811; BAA77289.1;
EMBL; AB013811; BAA77289.1;
EMBL; AB013812; BAA77289.1;
InterPro; IRR013842; Hemagalutn.
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                                                        Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAIN=72, 70, AND 71;
Nagashima M., Mori S., Sekine H.;
"Influenza A virus gene for hemagglutinin.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mori S., Sekine H.;
"HA1 domain of Influenza A (H3N2) virus.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB014062; BAA77294.1; -.
EMBL, AB013808; BAA77286.1; -.
EMBL, AB014060; BAA77292.1; -.
EMBL, AB014061; BAA77293.1; -.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLITININ (FRAGMENT).
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PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Pfam; PF00509; Hemagglutin.i. 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn: 1.
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Matches 9; Conservative
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95241;
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"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
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68.8%; Score 55; DB 12; Length 236; 100.0%; Pred. No. 0.25; or Mismatches 0; Indels
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Pred. No. 0.31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139937; AAD34854.1; -.
InterPro; IPR001364; Hemagglutn.
Pfam; PR00599; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
ProDom; PD000225; Hemagglutn; 1.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139336; AAD34853.1; ...
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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H3 HEWAGGLUTININ (FRAGMENT).
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EMBL, AF008782; AAB63719.1; -. InterPro.; IPRO01364; Hemagglutn. Pfam; PF00509; Hemagglutnin; 1. ProDom; PD000225; Hemagglutn; 1.
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STRAIN=A/TAIWAN/2191/96;
Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenza A virus (A/Taiwan/2191/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95236;
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Influenza virus A and B group; Influenza A viruses.
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STRAIN-4/ILLINDIS,
STRAIN-4/ILLINDIS,
FILCH W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF139932; AAD34849.1; -.
InterPro: IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutn.; 1.
Proloon; PD000229; Hemagglutn.; 1.
Proloon; PD000225; Hemagglutn.; 1.
NON_TER 1 1 1
NON_TER 286 286
SEQUENCE 286 AA; 31976 MW; 69AB2AE727D26078 CRC64;
                                                                                        286 286
286 AA; 32059 MW; CB51B092AAD0D7D8 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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PRO0329; HEMAGGLUTN12.
PD000225; Hemagglutn; 1.
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Best Local Similarity
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   PRINTS;
                                  ProDom;
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Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=147149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=A/FINLAND/583/98;
Pyhala R., Haanpaa M., Kleemola M., Tervahauta R., Visakorpi R.,
Kinnunen L.;
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                                                                           68.8%; Score 55; DB 12; Length 325; 100.0%; Pred. No. 0.36; Live 0; Mismatches 0; Indels
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID=11320;
325 AA; 36103 MW; 4E5B4648C2024765 CRC64;
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325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Vaccine 0:0-0(5001).
InterPro; IPR001364; Hemagglutn.
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Osiowy C.K.;
"Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus "Genetic characterization of A/Sydney/05/97-like(H3N2) Influenza virus isolates circulating in Canada during the 1997/98 Influenza season."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF087700; AAC36729.1; -...
InterPro; IPR001364; Hemagglutin.
Probom: PF000509; Hemagglutinin; 1.
Probom: P000225; Hemagglutinin; 1.
Probom: P000225; Hemagglutinin; 1.
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Pred. No. 0.36;
0; Mismatches 0; Indels
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Pred. No. 0.36;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBI_rexiD=11320;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity
9; Conserv?
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327 AA;
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Best Local Similarity
Matches 9; Conser
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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
               Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN'1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008787; AAB63724.1; -.
InterPro; IFR001364; Hemagglutin.
Probom; PE000255; Hemagglutinin; 1.
Probom; PE000225; Hemagglutini; 1.
Probom; P2000255; Hemagglutini; 1.
NON_TER 1 1
NON_TER 326 A8; 36197 MW; 4B84BD4AADC44A77 CRC64;
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STRAIN-A/PENNSYLVANIA/7/94(H3N2);
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-197) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008788; AAB63725.1;
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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NCBL_TaxID=11320;
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326 AA; 36197 MW; 4B84BD4AADC44A77 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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100.0%; Pred. No. 0.36;
iive 0; Mismatches 0
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STRAIN=A/NEW_YORK/28/94(H3N2);
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                                                                                                                                                                                   Query Match 68.8
Best Local Similarity 100.
Matches 9; Conservative
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326 AA;
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Generic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
Generic characterization of A/Sydney/05/97-like(H3N2) Influenza virus
1solates circulating in Canada during the 1997/98 Influenza season.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF087011, AAC35730.1;
InterPro: IPR001364; Hemagglutin.
Pfan, PF00509; Hemagglutinin: 1.
PRINTS; PR001229; Hemagglutinin: 1.
                                                                   Oslowy C.K.;
"Genefit characterization of A/Sydney/05/97-like(H3N2) Influenza virus
"Genefit characterization of A/Sydney/05/97-like(H3N2) Influenza virus
isolates circulating in Canada during the 1997/98 Influenza season.";
Submitted (ANG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF087709; AAC36738.1;
InterPro; IPR001364; Hemagglutin.
Probom: PD000225; Hemagglutin.; 1.
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Influenza virus A and B group; Influenza A viruses; Influenza A virus:
NCBI_TaxID=82372;
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                                                                                                                                                                                                                                                                                                                                                                                             68.8%; Score 55; DB 12; Length 327;
100.0%; Pred. No. 0.36;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.8%; Score 55; DB 12; Length 327; 100.0%; Pred. No. 0.36; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           327 327
327 AA; 36293 MW; 4A72007829B091F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 AA; 36373 MW; ADBD67D856EBCC96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenza A virus (A/Sydney/05/97-like(H3N2)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-A/SYDNEY/05/97-LIKE(H3N2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17, HEMAGGLUTININ (FRAGMENT).
                                              STRAIN-A/SYDNEY/05/97 (H3N2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEMAGGLUTININ (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
.-heq 9; Conserve
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 YPYDVPDYA 106
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YPYDVPDYA 9
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09YT89;
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09YT89
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Q9YT90
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os influenza A virus (A/Sydney/O5/97-11ke(H3N2)).

ov Viruses; ssRAR negative-strand viruses; Orthomyxoviridae;

ox Influenza virus A and B group; Influenza A viruses; Influenza A viruses.

ox NCBL_TaxID-82372;

RN | 11 |

RP | SEQUENCE FROM N.A. |

RC STRAIN-A/SYDNEY/O5/97-LIKE(H3N2);

RT | Genetic characterization of A/Sydney/O5/97-like(H3N2) Influenza virus RT |

Calouy C.K.;

Calouy C.K.;

Calouy C.K.;

RT | AGGIG1999 | to the EMBL/GenBank/DDBJ databases.

RT | Submitted (Aduc1999) to the EMBL/GenBank/DDBJ databases.

DR | RAMEN PRO0136; Hemagglutin. |

DR | FRINTS; PR00139; Hemagglutin. |

RT | NON_TER | 1 |

Ouery Match | 68.8%; Score 55; DB 12; Length 327; Best Local Similarity | 100.0%; Pred. No. 0.36; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps |

Oy | 1 | PPYDVPDYA 9 |

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DB | 98 YPDDVPDYA 106 |

Search completed: April 11, 2002, 10:22:57
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Haemagglutinin epi Haemagglutinin epi Haemagglutinin, HA Haemagglutinin epi Influenza haemaglu Truncated Human p? Truncated cyclin d Human cyclin depen Truncated Human p?

Human cyclin depen

Perfect score:

Run on:

Sednence:

Scoring table:

Searched:

Database

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Haemagglutinin; epitope; monoclonal antibody; detection; isolation; fusion protein.
                                                                                                                                                                                                                                                  Human influenza virus haemagglutinin epitope peptide fragment #3.
                                                                                                                                                                                                                                                                                                 /note= "N-terminal biotinoyl-epsilon-Aca group"
                                                                                                                                                                                                                                                                                                           /note= "C-terminal amide group"
                                                                                                                                                                                         ALIGNMENTS
                             AAY96048
AAY96075
AAY97530
AAY96045
AAY96072
AAB99371
                                                                                                                      AAB75004
AAB75005
AAB75006
AAB75010
AAB75010
AAB75012
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AAB75026
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     AAW73371
AAB73290
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AAB99395
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AAB99399
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               AAW73370
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                   AAB49724
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                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           Grol M, Hinzpeter M;
                                                                                                                                                                                                                    AAW59452 standard; peptide; 13
96DE-1043314
                                                                                                                                                                                                                                                                                                                                                      96DE-1043314
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                             Human parainfluenza virus.
WPI; 1998-241603/22
                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                      DE19643314-A1
                                                                                                                                                                                                                                         28-AUG-1998
                                                                                                                                                                                                                                                                                                                                           21-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                      21-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                           Emrich T,
AAW59452
.. ~!
                                                                                                                                                                                                                                                                                                                                Human influenza vi
Peptide encoded by
Flu-epitope scramb
Flu epitope tagged
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                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequenc
Saccharomyces cere
                                                                                                                                                                                                                                                                                                                                                           Influenza haemaggl
                                         (without alignments)
18.152 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                  Compact structure
                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                       Description
                                   April 11, 2002, 10:15:43; Search time 53.05 Seconds
                                                                                                                                                         PTAT-HA
                                                                                                                                                                                                                                                                                                                                                                            PTAT-HA
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                             522463 segs, 74073290 residues
                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                 AAW59452
AAB07730
AAW41032
AAW429116
AAB45969
AAY90725
AAY49751
AAB03963
AAB23443
AAG63443
AAG63443
                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                   SGSGYPYDVPDYA 13
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1. SGSGYPYDVPDYA
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Maximum DB seq length: 200000000
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481
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Match Length
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94.7
89.3
89.3
89.3
89.3
86.7
86.7
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75 67 67 67 67 67 65 68 68

26432

Score

Result No.

Anti-ILB monoclona Anti-ILB monoclona

Human interleukin Human interleukin

Length 34;

94.7%; 92.3%;

Similarity

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Gaps

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This peptide fragment represents a human influenza virus haemagglutinin epitope which is used to make monoclonal antibodies with an affinity constant of 108 M·1. Such antibodies are used for detecting and isolating native human influenza virus haemagglutinin (HA), modified HA or HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elements encoding a gene product with a desired activity. Expression of the genetic element results, directly or indirectly in the modification of an optical property of the encoded polypeptide. The method comprises compartmentalizing the genetic elements into microcapsules, expressing them to produce their respective gene products within the microcapsules, and sorting genetic elements which produce the gene product(s) with the desired activity. The method is used for isolating genetic elements which encode a gene product with a desired activity. This can be a represents a fusion of a flag epitope and influenza haemagulutinin. It was used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a method for isolating one or more genetic
                 virus haemagglutinin - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolation of genetic elements encoding a gene product with a desired activity is carried out in microcapsules where changes in optical activity are detected -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide encoded by amplification product encoding a FLAG-HA peptide.
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic element; optical property; gene product; microcapsule.
                                                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                  100.0%; Score 75; DB 19;
100.0%; Pred. No. 1.6e-05;
Live 0; Mismatches 0;
               Monoclonal antibodies to influenza virus haemagg
detecting and isolating haemagglutinin proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; Page 79-80; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB07730 standard; Peptide; 34 AA.
                                                                Claim 7; Page 2; 6pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JAN-2000; 2000WO-GB00030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99GB-0000298
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Griffiths A, Tawfik D;
                                                                                                                                                                                                                                                                                                                                                   1 sgsgypydvpdya 13
                                                                                                                                                                                                                                                                                                                       SGSGYPYDVPDYA 13
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N-PSDB; AAA59266.
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                     13 AA;
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                                                                                                                                                                    fusion proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                     Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAB07730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a scrambled flu-epitope peptide, and can be used in the method of the invention. The method is for screening for transdominant bloactive agents (A) abbe to alter the phenotype of a comprises: (a) introducing a library of different randomised nucleic acids (I) into cells; and (b) screening the cells for altered phenotype due to presence of (A). (A) are potential pharmaceuticals, from their effect on signalling pathways. A particular application is to identify peptides, encoded by (I), that have antitumour activity or are able to increase sensitivity to, or reduce toxicity of, known antitumour agents. More generally the method can identify agents for treatment of many other conditions, e.g. cardiovascular diseases, anglogenesis, atherosclerosis, obesity, neurodegeneration, bone disease, viral and other infections,
                                                                                                                                                                                                                                                                                                     Transdominant bioactive agent, phenotype alteration, signalling pathway, antitumour agent; cardiovascular disease; angiogenesis; atherosclerosis; obesity; neurodegeneration; bone disease; infection; allergy; therapy;
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening for trans-dominant active agents able to alter phenotype - useful to identify potential drugs with e. g. anti-tumour activity
                               Indels
Score 71; DB 21;
Pred. No. 0.00018;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                          AAW41032 standard; Protein; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 53; 91pp; English.
                               ö
                                                                                                                                                                                                                                                                         Flu-epitope scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US01048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0589911.
96US-0589109.
                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 89.3
Best Local Similarity 91.7
Matches 11; Conservative
                                                             SGSGYPYDVPDYA 13
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                                                                                                                                                                                                                                                                                                                                                        flu-epitope peptide.
                                                                                Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-1996;
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Query Match
Best Local Simi
Matches 12;
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                                                                                                                                             RESULT
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2 GSGYPYDVPDYA 13

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WO9727212-A1.

Synthetic.

AAW29116;

RESULT AAW29116

a

31-JUL-1997.

23-JAN-1997;

23-JAN-1996;

Noaln GP;

activity

23-JAN-1996;

Thu Apr 11 15:31:13 2002

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This invention describes novel in vitro screening methods (1) for a transdominant intracellular bloactive agent capable of altering the phenotype of a cell. (1) comprises: (a) introducing a molecular library of randomized candidate nucleic acids into several cells; and (b) screening the cells for a cell exhibiting an altered phenotype, where the altered phenotype is due to the presence of a transdominant bloactive agent. The methods are particularly useful for screening intracellular transdominant effector peptides and RNA molecules selected inside living cells from randomized pools. (1) is also useful for introducing random libraries into cells to screen for bloactive compounds. The methods allow rapid and highly efficient screening of large numbers of random cligonucleotides and their corresponding expression products in a single step. In addition, the methods allow screening in the absence of significant prior characterization of the cellular defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methods for screening intracellular transdominant effector peptides and RNA molecules comprise delivering random oligonucleotides to cells, which are then screened for an altered phenotype
                                                                                                                                                                                                                                                          Intracellular transdominant bloactive agent; screening; cell phenotype; effector peptide.
                                                                                                                                                                                                                     Transdominant effector peptide associated screening peptide #49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 67; DB 22; Length 17; Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Column 79-80; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STRD ) UNIV LELAND STANFORD JUNIOR. (RIGE-) RIGEL PHARM INC.
                                                                        AAB45969 standard; Peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY90725 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0789333.
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96US-0589911
                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rothenberg SM, Nolan GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 89.3
Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AA;
                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-1996;
                                                                                                                                                                     02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                        US6153380-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2000
                                                                                                                     AAB45969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY90725;
                         RESULT
AAB45969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY90725
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                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This peptide comprises a Flu epitope tagged scrambled peptide.

Wurine 1071/2 Clone 8 cells were infected with pBabe puro retrovirus constructs containing a sequence coding for the Flu scrambled epitope or an inhibitor peptide (see AAW2917) identical cortambled epitope or an inhibitor peptide (see AAW2917) identical scrambled epitope or an inhibitor peptide (see AAW2917) identical to the C2 region of protein kinase C (PKA) isozymes. Control clone of colls showed predominantly cytoplasmic and periluclear staining. Those infected with constructs coding for the C2 region showed predominantly cytoplasmic and periluclear staining in both control and PWA induced cells. Novel outcomes can staining in both control and PWA induced cells. Novel outcomes can cocur upon expression of peptides in cells. A claimed method of screening for transdominant intracellular bioactive agents (A) able to alter the phenotype of a cell comprises: (a) introducing a library of different randomised nucleic acids (I) introducing a containing the cells for altered phenotype due to presence of containing the cells for altered phenotype due to presence of alfferent randomised (I); and (2) a library of ammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening for transdominant intracellular active agents able to alter cell phenotype - useful for examining for changed phenotype, particularly to identify potential drugs with e. g. antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                          Transdominant intracellular effector peptide; RNA; screening; altered phenotype; retrovirus; library; signal transduction; antitumour; pBABE; influenza virus; flu; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing the library of (1), preferably integrated into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
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Pred. No. 0.00038;
0; Mismatches 1;
                                                                                                                                                                                                                                                               Flu epitope tagged scrambled peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 53; 91pp; English.
                                                                                                                   AAW29116 standard; Peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US01019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0589911
96US-0589109
                                                                                                                                                                                                                04-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GSGYPYDVPDYA 13
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2 gggypydvpdya 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-393611/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AA;
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Gaps

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1; Indels

Sequence

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16-AUG-2000 (first entry)

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0
                        Fusion; scaffold protein; peptide library; green fluorescent protein; GFP; self-binding; detection; cellular expression; screening; catabolism.
                                                                                                                                                                                                                                                           Fusions of scaffold proteins with random peptide libraries for improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises the influenza haemagilutinin (HA) epitope tag embedded with glycines, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compact structure forming peptide; dimerisation; stability; scaffold; library screening; drug screening; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Influenza haemagglutinin epitope tag containing 19mer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%; Score 67; DB 21; Length 19; 91.7%; Pred. No. 0.00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compact structure forming exemplification peptide #44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                             Peelle BR;
                                                                                                                                                                                                                                                                                               Example 2; Page 80; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY49751 standard; peptide; 38 AA.
                                                                                                                                                                                                             Bogenberger JM,
                                                                                                                                                            98US-0169015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                     (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GSGYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 gggypydvpdya 13
                                                                                                                                                                                                                                   WPI; 2000-303765/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                       library screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AA;
                                                            Influenza virus.
                                                                                   40200020574-A2
                                                                                                                                                            38-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9951625-A2
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                                                                                                             13-APR-2000.
                                                                                                                                                                                                             Anderson D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY49751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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AAY49751
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The present invention describes peptides which have a moderate or high affinity for each other, when added as extensions to both the N-terminus and C-terminus of a protein, can be used to help fold the protein into a compact structure. This compact structure is more stable to proteases. A composition (A) comprises at least a first dimerisation peptide (I) comprising the sequence (S1) that is no more than 8 amino acids long, where the composition optionally comprises a second dimerisation peptide (II): NH2-X1-X2-X3-X4-X5-COOH (S1) where X1 to X4 = Ala, Val, Ile, Leu, Trp, Phe, Met, or Try, and X5 = Lys, Arg, Asp or Glu; NH2-X1-X2-X3-X4-X5-COOH (II). The compositions of the invention are displayed intracellularly or extracellularly and are useful to identity binding proteins and molecules, and to modulate intracellular signalling pathways. A library of constrained proteins may be evaluated in vivo for its bloactive potential. The invention can be used to access molecules its bloactive potential. The invention be used to access molecules or tragets within living cells, and then provide for the isolation of the constrained protein which has a phenotypic effect on the living cells. The methods are also useful to identify in vitro binding partners of the constrained protein. The compositions of the invention are useful in physiological fluids. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel dimerization peptides which self-associate are used with other proteins to effect the formation of compact structures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 0.00087;
0; Mismatches 1; Indels
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ilarity 91.7%;
Conservative (
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                                                                                                                                                 98US-0080444.
                                                                          99WO-US07374
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 AA;
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                                                                                                                                                                                                                            RIGE-) RIGEL
                                                                          02-APR-1999;
14-OCT-1999
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                                                                                                                                                                                                                                                                                                       Anderson D;
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99US-0122757.

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Fusion molecules comprising protein transduction domains and therapeutic agents, useful for treating e.g. Alzheimer's and Parkinson's diseases, dementia and epilepsy -
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                 Human immunodeficiency virus
                                                                                                                                                               28-FEB-2000; 2000WO-US05097.
                                                                                                                                                                                                                                                                       (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-647439/62.
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC63859
                                                                             WO200062067-A1.
                                                                                                                                                                                                         28-FEB-1999;
29-AUG-1999;
                                                                                                                       19-OCT-2000
                                     Synthetic
                                                                                                                                                                                                                                                                                                                   SF;
                                                                                                                                                                                                                                                                                                                   Dowdy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-apoptotic polypeptide which comprises a portion of an anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in combination with a transport group is described. The transport group is capable of transporting the chimaric group or fusion peptide across the cell membrane. The anti-apoptotic polypeptide is FLICE-like inhibitor protein (FLIP) which inhibits Fas and TWF mediated apoptosis by inhibiting binding of Caspase 8 to the Fas receptor complex, thus shutting off the downstream Fas signalling pathway. The chimaric group and fusion peptide are useful for inhibiting ligand-induced apoptosis by bringing them into contact with T cells. The chimaric group is useful for expanding T cells in vitro e.g. T cells specific for particular antigens such as tumour-specific antigen, for enhancing particular antigens such as tumour-specific antigen, for enhancing T cells e.g. activated CD4+ T cells in HIV infected patients. The chimaric group is also useful for therapeutic, prophylactic or classical propertides and macromolecules such as anti-apoptotic polypeptides and nucleic ancoding such polypeptides. Two primers (AAA54298) were cased to amplify the FLIP CDNA for subcloining into the Xhol-Nool stream for the pHA-TAT vector which contains the N-terminal protein transduction domain from the human immunodeficiency virus tat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein transduction domain; fusion molecule; therapeutic agent; drug targetting; drug discovery; cell transduction; bioavailability; vaccine; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy; seizure; compulsive behaviour; meningitis; encephalitis; ischaemia; spongiform encephalopathy; dyslexia; age-related memory loss; Lou Gehring's disease; viral infection; HIV; bacterial infection.
                                                                                                                                                                                                                                                                                                                 Fusion polypeptide useful for inhibiting ligand-induced apoptosis, comprises portion of anti-apoptotic polypeptide linked to a transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein. Tat is a preferred transport moiety.
                                                                                                                       (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB29443 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pTAT-HA linker-encoded peptide.
                                                                                                                                                                                                           Paya C, Algeciras-schminich A;
                                                                                                                                           (PAYA) PAYA C. (ALGE/) ALGECIRAS-SCHMINICH A.
               05-APR-2000; 2000WO-US09002.
                                                         99US-0127867
99US-0128021
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Matches 11; Conservative
                                                                                                                                                                                                                                                   WPI; 2000-664988/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SGYPYDVPDYA 13
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2 sgypydvpdya 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AA;
                                                                                                                                                                                                                                                                         N-PSDB; AAA54300
                                                         05-APR-1999;
06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                group
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The invention relates to a novel fusion molecule comprising at least one protein transduction domain (PTD) and at least one linked molecule has therapeutic or prophylatic activity against a medical condition. The invention also relates to methods of drug discovery in which the test compound is linked to a suitable transducing protein and introduced to a cell; a method of Killing reasonable protein and introduced to a cell; a method of Killing comprising a covalently linked fusion molecule; and a mammal adapted for experimental use in which at least one transduction molecule; a mammal compensation which at least one transduction molecule has been transduced into essentially all the cells of the mammal. The fusion molecule is used to deliver a therapeutic agent to a mammal, especially a human. The linked molecule may be a vaccine, an anti-infective drug, a cardiovascular drug, an antitumour drug, an antitumour drug, an antitumour drug, an antitumour drug or the treatment or prevention of a central or peripheral nervous system discase, Huntington's disease, and also includes pre-senile central nervous system (CNS) disorder is especially Alzheimer's disease. Parkinson's disease, Huntington's disease, and also includes pre-senile dementia, epilepsy and seizures, compulsive behaviour, meningilis.

Concluding viral and bacterial meningitis), encephalitis, ischemia, crapple (or related spongiform encephalopathies), dyslexia, age-related menning vioss or Lou Gehring's disease. Rusion molecules can also be used to kill virally infected cells, especially those infections. The methods are a highly effective means for transducing a molecule of into an entire mammal or into specific cells, tissues, organs and seizue within it. They also overcome bloavailability problems that are associated with many therapeutic agents (e.g., large molecules or are associated with many therapeutic agents (e.g., large molecules or experienced transduction of the transduction of the transgences; or the represents a protein transduction domain u
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:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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ID AAG6
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(BRBI-) BRITISH BIOTECH PHARM LTD.
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ilarity 90.9%;
Conservative
 96GB-0006126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemagglutinin epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-489648/45.
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Best Local Similarity
Matches 10; Conserv
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                                                                                              N-PSDB; AAT85308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemagglutinin.
 22-MAR-1996;
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                                                      Edwards RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW73372;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a chimeric fusion protein of the invention. The specification describes a chimeric pIX protein having at least one adenoviral pIX domain and a non-native amino acid sequence. The non-native sequence is a ligand that binds to a substrate present on surface cells. The chimeric proteins are used for producing adenovirus
                                                                                                                                                                                                                                                                                                                                                           Chimeric pIX protein useful in an adenovirus gene transfer vector for infecting cells comprises at least one adenoviral pIX domain and a non-native amino acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha mating factor receptor; Ste2; mutant; biosensor; diagnosis; G-protein coupled receptor; GPCR; environmental monitoring; on-line process monitoring.
                                                      Amino acid sequence of C-terminal fusion protein of pIX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.0%; Score 64.5; DB 22; Length 165; 92.9%; Pred. No. 0.0098; tive 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae alpha mating factor receptor Ste2.
                                                                                pIX protein; chimeric protein; gene transfer vector
                                                                                                                                                                                                                                                                                          Wickham TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 27-28; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW27158 standard; Protein; 481 AA.
                                                                                                                                                                                                         09-FEB-2001; 2001WO-US04233.
                                                                                                                                                                                                                                    09-FEB-2000; 2000US-0181163.
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                           (first entry)
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                                                                                                                                                                                                                                                                                        Roelvink PW, Kovesdi I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene transfer vectors.
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N-PSDB; AAH74659.
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 AA;
                                                                                                                          Mastadenovirus.
                                                                                                                                                   WO200158940-A2.
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                           15-OCT-2001
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                                                                                                             Synthetic.
AAG63606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF, TBP associated factor; TAF-interaction factor; gene expression regulator;
                                                                                                                                                                                                                                                                                                                         mating factor receptor Ste2, which was used in the development of a method to prepare cells presenting on their surface a mutant of a method to prepare cells presenting on their surface a mutant of a protein coupled receptor (GPCN) binding a desired ligand which the natural receptor cannot. The method comprises generating to replicable expression plasmids comprising a coding sequence for a GPCN mutated by one or more amino acids in its transmembrane and/or extracellular domains, and operatively linked expression control sequences, transforming host cells with the plasmids and contacting the cells with the ligand and isolating those which bind. GPCN are natural receptor proteins, i.e. membrane proteins that allow cells to detect molecules in the extracellular environment. Cells presenting mutant GPCN on their surfaces are useful as biosensors, with potential applications in diagnostics and environmental and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Cells for surface expression of mutants of natural G-protein receptor - where the mutants can bind a ligand that the natural receptor cannot, useful as biosensors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 0.073;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               The present sequence is the Saccharomyces cerevisiae alpha
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                                                                                                                                                                                                    Example 1; Pages 13-15; 35pp; English.
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This sequence represents a haemagglutinin epitope. It was used in an epitope-tagged TATA-box binding protein (TBP) that is expressed by the transgents on-human animals of the invention. The animals are used to produce TBP. TBP is used to isolate and characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific TBP associated factors (TAFs, e.g. transcription factors, activators or inhibitors) and TAF-interaction factors, and to raise antibodies against TBP. The TAFS may be useful for regulating gene antibodies against TBP. The TAFS may be useful for regulating gene antibodies are used for affinity purification of TBP and its complexes. TBP can isolate transcription complexes from a wide variety of different tissues and cells (contrast known methods that are limited to isolation complexes from a particular cell type).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.3%; Score 61; DB 20; Length 10; 100.0%; Pred. No. 0.0019; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0%; pred. No. 0.0
Matches 10; Conservative 0; Mismatches
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                                                                                        Claim 17; Page 18; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemagglutinin epitope
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                                                        therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gypydvpdya 10
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                                                                                                                                                                                                                                                                                                                                                                                                                   10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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This sequence represents a haemagglutinin epitope. It was used in an

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transgenic non-human animals of the invention. The animals are used to transgenic non-human animals of the invention. The animals are used to produce TBP. TBP is used to isolate and characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific TBP associated factors (TARS, e.g. transcription factors, activators or inhibitors) and TAP-interaction factors, and to raise antibodies against TBP. The TAFS may be useful for regulating gene expression, e.g. disease-related genes, so are potential pharmaceuticals, also for identifying human analogues for use in drug screening. The antibodies are used for affinity purification of TBP and its complexes. TBP can isolate transcription complexes from a wide variety of different forms and cells contrast known methods that are limited to isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to transgenic mice comprising a transgene under operational control of a myocyte-specific promoter. The transgene encodes a protein having wild-type CREB activity or dominant negative CREB activity. CREB is 4 3 kD basic leucine zipper transcription factor. The expression of the transgene leads to congestive heart failure (CHF). The transgenic mice are useful as genetic models of dilated cardiomyopathy or phenotypes associated with CHF. The transgenic mice are also useful for providing important basic information concerning the role of the CREB transcriptional pathway in regulating cardiac mycocyte function. These animals will also facilitate studies designed to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic mice expressing CREB, useful as genetic models for congestive heart failure, e.g. progressive biventricular failure, cardiac dilation, decreased myocardial contractility, peripheral edema or intracardiac thrombi
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREB; HA peptide tag; transgenic mouse; transcription factor; congestive heart failure; CHF; haemagglutinin.
                                                                                                                                                                                                                                                                                                                                                              Score 61; DB 20; Length 11; Pred. No. 0.0021; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                          81.3%; Score ~.,
100.0%; Pred. No. 0.00
".... 0; Mismatches
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                                                                                                                                                                                                                                                                    from a particular cell type).
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Influenza virus
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                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a haemagglutinin epitope. It was used in an epitope-tagged TATA-box binding protein (TBP) that is expressed by the transgenic non-human animals of the invention. The animals are used to produce TBP. TBP is used to isolate and characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific TBP associated factors (TAFS, e.g. transcription factors, antibodies against TBP. The TAFS may be useful for regulating gene expression, e.g. disease-related genes, so are potential pharmaceuticals, also for identifying human analogues for use in drug screening. The ran isolate transcription complexes from a wide variety of different tissues and cells (contrast known methods that are limited to isolation
new drugs that can decrease the morbidity and mortality associated with the disease. The present sequence is influenza haemagglutinin (HA) peptide tag, which was used in the present invention.
                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                   81.3%; Score 61; DB 22; Length 11; 100.0%; Pred. No. 0.0021; 1ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                     Best_Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       4 GYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                                                                                                                              11 AA;
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                                                                                                                                    Sequence
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81.3%; Score 61; DB 20; Length 12;

Query Match

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Gaps
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                      Indels
Pred. No. 0.0023;
                                                                                                                    Search completed: April 11, 2002, 10:15:44
Job time: 94 sec
                      ;
           100.08;
          Best Local Similarity 100. Matches 10; Conservative
                                              4 GYPYDVPDYA 13
                                                          2 gypydvpdya 11
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Sequence 52, Application US/09169015
Patent No. 6180343
GENERAL INFORMATION:
APPLICANT: Anderson, David
TITLE OF INVENTION:
TITLE OF INVENTION Green Fluorescent Protein Fusions with Random Peptides
FILE REFERENCE: A66900/DJB/RMS/SJR
CURRENT APPLICATION NUMBER: US/09/169,015
CURRENT FILES 1998-10-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
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US-08-789-333F-51
       Sequence Seq
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US-08-478-386A-19
US-08-25-597-19
US-08-46-498-6
US-08-388-653-19
US-08-388-653-19
US-08-690-011A-17
US-08-690-011A-17
US-08-690-011A-49
US-08-687-559-14
US-08-687-559-14
US-08-748-19
US-08-813-19
US-08-813-19
US-08-813-818-28
US-08-813-818-28
US-08-813-818-28
US-08-818-818-819
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US-08-818-818-819
US-09-157-753-19
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Best Local Similarity 91.7
Matches 11; Conservative
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US-09-169-015-52
              TYPE: PRT
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Sequence 15,
Sequence 4, 1
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Sequence 6
Sequence 6
Sequence 6
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-169-015-52

US-09-2208-966-15

US-09-2208-966-15

US-09-2208-966-15

US-08-632-514C-29

US-08-634-060-27

US-08-672-213-39

US-08-672-213-39

US-08-199-780-1

US-08-199-199-19

US-08-101-3988-6

US-08-101-3988-6

US-08-101-3988-6

US-08-101-3988-6

US-08-101-3988-6

US-08-167-982-1

US-08-167-982-1

US-08-167-982-1

US-08-634-060-31

US-08-634-060-31

US-08-461-859-6

US-08-461-859-6

US-08-461-859-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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SEQUENCE CHARACTERISTICS
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                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                          2 GYPYDVPDYA 11
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Best Local Similarity
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APPLICANT: Leiden, Jeffery M
TITLE OF INVENTION: DILATED CARDIOMYOPATHY IN TRANSCENIC MICE EXPRESSING A
TITLE OF INVENTION: DILATED CARDIOMYOPATHY IN TRANSCRIPTION FACTOR IN THE
TITLE OF INVENTION: HEART
TITLE OF INVENTION: HEART
CURRENT PAPLICATION NUMBER: US/09/215,098
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/068,011
PRIOR FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF FILE REPERENCE: 48811/1742
CURRENT APPLICATION NUMBER: US/09/208,966
CURRENT FILING DATE: 1998-12-10
EARLIER APPLICATION NUMBER: 60/082,402
EARLIER FILING DATE: 1998-04-20
EARLIER APPLICATION NUMBER: 60/069,012
EARLIER FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTI Ver. 2.0
SEQ ID NO 15
LENGTH: 16
                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-169-015-52
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                                                                                                                                                                            Length 19;
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                                                                                                                                                                          Score 67; DB 4; I
Pred. No. 0.00013;
0; Mismatches 1;
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Patent No. 6194632
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SEQ ID NO 52
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
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91.7%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                11; Conservative
                                                                                                                                                                                                                                                                           2 GGGYPYDVPDYA 13
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Best Local Similarity
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; ORGANISM: human
US-09-208-966-15
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US-09-215-098-4
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LENGTH: 11
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             Length 11;
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                                                                                                                                                                                                                                                                                                                  APPLICANT: GALLO, Gregory J.
TITLE OF INVENTION: APOPTOSIS ASSOCIATED PROTEIN BBK
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-188-177-29
Sequence 29, Application US/09188177
Sequence 29, Application US/09188177
Sequence 29, Application US/09188177
Sequence 29, Application US/09188177
Sequence 20, Application US/09188177
Sequence 20, Gregory J.
TITLE OF INVENTION: APOPTOSIS ASSOCIATED PROTEIN BBK
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,514C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.3%; Score 61; DB 2; Le
100.0%; Pred. No. 0.0008;
iive 0; Mismatches 0;
             Score 61; DB 4; Le
Pred. No. 0.00062;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104322.188
                                                                                                                                                                                                                                US-08-632-514C-29; Sequence 29, Application US/08632514C; Patent No. 5834234; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
81.3%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: WIXON, Henry N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 10f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)942-8484
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202)942-8459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 14 amino acids TYPE: amino acid
                                                        Conservative
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Gaps

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APPLICANT: WICKHAM, THOMAS J.
APPLICANT: ROBLYINK, PETRUS W.
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
TITLE OF INVENTION: USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 Score 59, DB 1; Length 25; Pred. No. 0.0031; 2; Indels 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 59; DB 2; Length 25;
Pred. No. 0.0031;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTR: 1.0
CUDNITR: 1.0
COUNTR: 0.0
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDTUM TYPE: FICHOPY disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,846
FILING DATE: Z1-AUG-1996
CLASSIFICATION: 514
ATONERY/AGENT INFORMATION:
NAME: LARCHER. CAROL
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 35243
FELECOMMUNICATION INFORMATION:
TELEPRAX: (312) 616-5600
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHRRACTERISTICS:
SEQUENCE CHRRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 10, Application US/08700846; Patent No. 5962311; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.7%;
83.3%;
                                                                                                                                                                                                                                     78.78;
83.38;
TELEFAX: (312) 616-5700 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.7
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                     Query Match 78.7
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-634-060-27
                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide US-08-700-846-10
                                                                                                                                                                                                                                                                                                                         2 GSGYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                                                                 2 GSGYPYDVPDYA 13
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                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-08-700-846-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: STATE:
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APPLICANT: Kovesdi, Imre
APPLICANT: Roelvink, Pertus W.
TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY
TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN
CORRESPONDENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.3%; Score 61; DB 3; Length 14; 100.0%; Pred. No. 0.0008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/09/188,177
FILING DATE: 2
CLASSIFICATION:
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
ATTONEY/AGENT INFORMATION:
TELEPHONE: (202)942-8489
TELEPHONE: (202)942-8489
TELEPHONE: (202)942-8489
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
"""""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Leyolig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: 11110018
COUNTRY: USA
ZID: 60601
COMPUTER: ELAPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,060
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,162
FILING DATE: 08-SEP-1994
CLASSIFICATION: 514
ATONNEY/AGENT INFORMATION:
NAME: K11yk, John Jr.
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71602
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/08634060 Patent No. 5712136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 81.3
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-188-177-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GYPYDVPDYA 13
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             COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPOTER: LEM PC compatible
COMPOTER: LEM PC compatible
COMPOTER: TEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIFICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION NUMBER: US 60/019,614
FILING DATE: 27-JUN-1995
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
APPLICATION NUMBER: 31,235
REGISTRATION NUMBER: 31,235
REGISTRATION INFORMATION:
TELEPRAK: 617-494-0A00
TELEPRAK: 617-494-0A00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bondaio, Jeffrey
APPLICANT: Bondaio, Steven A.
TITLE OF INVENTION: Gene Transfer Into Bone Cells
TITLE OF INVENTION: And Tissues
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/199,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 59; DB 4; Le
Pred. No. 0.0052;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/199,780
FILING DATE: 18 FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David
REGISTATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC:002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (512) 320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08199780 Patent No. 5763416 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.7
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-672-213-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SGYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SSYPYDVPDYA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-199-780-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.7%; Score 59; DB 4; Length 27; 90.9%; Pred. No. 0.0034;
                                                                                                         APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08672213
Patent No. 6306649
GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
TITLE OF INVENTION: FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Gene Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIETCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: 31,235
REFERENCE/COCKET NUMBER: 31,235
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          ADDRESSEE: ARIAD Gene Therapeutics, Inc. STREET: 26 Landsdowne Street CITY: Cambridge STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: ARIAD Gene Therapeutics, Inc.
26 Landsdowne Street
                                                                                                                                                                                                                                                                                                                                              ZIP: 02139-4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 39, Application US/08672213 Patent No. 6306649 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.7
Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-672-213-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 20 ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SSYPYDVPDYA 13
                                                                                                                                                                                                                                                                                                                                     USA
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                US-08-672-213-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-672-213-29
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STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                 COUNTRY:
RESULT
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В

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Gaps
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18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09066074

Patent No. 5952467

APPLICANT: Hunter et al., Tony
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: Pat.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Parker, David L.
REGISTRATION NUMBER: 32.165
REFERENCE/DOCKET NUMBER: UMICO09P--
TELECOMUNICATION INFORMATION:
TELEPAX: (713) 789-2679
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acids
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83.3%; Pred. No. (
                                                                                                                          Sequence 1, Application PC/TUS9502251
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CELLS
HUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDORESSEE:
ADDRESSEE: APO Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                      Texas
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
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                       406 GCRYPYDVPDYA 417
   2 GSGYPYDVPDYA 13
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                                                                                                                                                                                                                                                                                                   Houston
                                                                                                                                                                                                                                                                                                                                      COUNTRY: Ur
ZIP: 77210
                                                                                             RESULT 13
PCT-US95-02251-1
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Pred. No. 0.095;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                             2; Indels
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COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/316,650

FILING DATE: 30-SEP-1994

CLASSIFICATION STAT:

APPLICATION NUMBER: US 08/199,780

FILING DATE: 30-SEP-1994

ATTORNEY AGENT INFORMATION:

NAME: PATKET, DAVID L.

REGISTRATION NUMBER: 32.165

REFERENCE/DOCKET 13.04

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 418-3000

TANNE: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08316650

Sequence 1, Application US/08316650

Patent No. 594449

GENERAL INFORMATION:

APPLICANT: Bonadio, Jeffrey

APPLICANT: Roesaler, Blake J.

APPLICANT: Goldstein, Steven A.

APPLICANT: Lin, Wushan

TITLE OF INVENTION: METHODS AND COMPOSITIONS

TITLE OF INVENTION: METHODS AND COMPOSITIONS

TITLE OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: ARNOLd, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: Texas

COUNTRY: USA
                                                                                                                                                                                                        Score 58; DB 1
Pred. No. 0.095
0; Mismatches
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 417 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                        Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 417 amino acids TYPE: amino acid
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                                                                                                              TOPOLOGY: 11near
MOLECULE TYPE: protein
US-08-199-780-1
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Best Local Similarity
Matches 10; Conserva
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Search completed: April 11, 2002, 10:14:44 Job time: 34 sec
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,074
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08555912A
Patent No. 5972697
GENERAL INFORMATION:
APPLICANT: Hunter et al., Tony
TILE OF INVENTION: NIMA INTERACTING PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Sulte 1400 CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
FILING DATE:
APPLICATION NUMBER: US 08/555,912
FILING DATE: 13-NOV-1995
ATTOWNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 07251/011001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TENERAL SEQUENCE CHARACTERISTICS:
TENERAL SEQUENCE CHARACTERISTICS:
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
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Best Local Similarity 81.87
Local 9; Conservative
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CLONE: PGAL-PIN1
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STATE: Cl
COUNTRY:
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COUNTRY:
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Gaps
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REFERENCE/DOCKET NUMBER: 07251/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLEGULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: PGAL-PIN1
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81.8%;
                                : 619/678-5070
619/678-5099
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Run on:

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hemagglutinin - influenza A virus (isolate A/Guangdong/25/93) (fragment)
C;Species: influenza A virus
A;Variety: isolate A/Guangdong/25/93
A;Variety: isolate A/Guangdong/25/93
C;Accession: S52188
R;Ellis, J. S.
Submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
552191
C.Species: Influenza A virus (isolate A/Hong Kong/2/94) (fragment)
C.Species: Influenza A virus
C.Species: Influenza A virus
A:Variety: isolate A/Hong Kong/2/94
C.Sate: O7-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C.Sate: O7-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
R.Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Reference number: S52173
A;Reference number: S52173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-347 <ELL>
A; Cross-references: EMBL:246408; NID:g609055; PIDN:CAA86543.1; PID:g609056
A; Experimental source: isolate A/Hong Kong/2/94
C; Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:246406; NID:9609049; PIDN:CAA86541.1; PID:9609050 A;Experimental source: isolate A/Guangdong/25/93 C;Superfamily: influenza virus hemagglutinin
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Pred. No. 0.17;
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Pred. No. 0.17;
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A; Molecule type: mRNA
A; Residues: 1-347 <ELL>
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Matches 10; Conserv
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                                                                                                                                                April 11, 2002, 10:16:16 ; Search time 27.06 Seconds (without alignments) 36.595 Million cell updates/sec
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Compugen Ltd.
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                          version .
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
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                                                                                                                                                                                                                                                                                                   SGSGYPYDVPDYA 13
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1 SGSGYPYDVPDVA
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length: 2000000000
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Perfect score:
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C; Superfamily: influenza virus hemagglutinin
C; Superfamily: influenza virus hemagglutinin; homotrimer; lipoprotein; thiolester bond
C; Keywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
F; 1-16/Domain: signal sequence #status predicted <HA1>
F; 345-565/Product: hemagglutinin HA1 #status predicted <HA2>
F; 345-555/Domain: transmembrane #status predicted <TMA>
F; 385-551/Domain: transmembrane #status predicted <TMA>
F; 387-337,53,68,78,180,300,480,310,480,310,480,310,430,440,481,67-292,79-91,154,488,296-320/Disubilide bonds: #status predicted
F; 554,561,564/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: JQ2374
R;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518
A;Title: Comparison of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtain A;Reference number: JQ2369; MUID: 94065682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemagglutinin - influenza A virus (strain SN1389 and IN0190)
C;Species: influenza A virus
C;Species: influenza A virus
C;Date: 14-Vul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: JQ2375; JQ2376
E;Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtain
                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: genomic RNA
A;Residues: 1-565 <KAW>
A;Cross-references: GB:M24727; GB:J04336; NID:g324000; PIDN:AAA43102.1; PID:g324001
                                                       hemagglutinin precursor - influenza A virus (strain A/equine/Kentucky/2/86[H3N8])
N:Contains: hemagglutinin HAI; hemagglutinin HA2
C;Species: influenza A virus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 16-Jul-1999
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C;Species: influenza A virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
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                                                                                                                                                                          C,Accession: A34065
R;Kawaoka, Y.; Bean, W.J.; Webster, R.G.
W;Irology 169, 283-292, 1989
A;Title: Evolution of the hemagglutinin of equine H3 influenza viruses. A;Reference number: A34064; MUID:89204899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 0.28;
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0.23;
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A;Residues: 1-330 <ROC>
A;Cross-references: GB:L20115
Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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Pred. No.
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69.28;
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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J. Gen. Virol. 72, 2007-2010, 1991
A;Title: Molecular evidence for a role of domestic ducks in the introduction of avian H3
A;Reference number: JQ1153; MUID:91341491
                                                                                                                                                                                                                                                                                                                           Virology 162, 160-166, 1988
AyItle: Origin of the hemagglutinin gene of H3N2 influenza viruses from pigs in China.
A;Reference number: A94370; MUID:88101364
A;Accession: A29971
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: genomic RNA
A;Residues: 1-550 <KID>
A;Cross-rreferences: GB:M19056; NID:g324208
A;Note: the sequence in GenBank entry FLAHAPA, release 106, (PID:g324209) differs from
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hemagglutinin precursor – influenza A virus (strain A/duck/Hong Kong/7/75) (fragment) N;Confrains: hemagglutinin HA1; hemagglutinin HA2 N;Species: influenza A virus C;Species: influenza A virus C;Date: 31-Mar_1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
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F:330-545/Product: hemagglutinin HA2 #status predicted <HA2>
F:8,22,38,165,285,483/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. Map position: segment 4
C. Superfamily: influenza virus hemagglutinin
C. Seywords: glycoprotein; hemagglutinin; homotrimer; lipoprotein; thiolester bond
C. Seywords: glycoprotein; hemagglutinin HAI #status predicted <HAI>
F. 13.08-Froduct: hemagglutinin HAZ #status predicted <HAI>
F. 520-536/promain: transmembrane #status predicted <HAZ>
F. 520-536/pomain: transmembrane #status predicted <MAZ>
F. 52. 38.165, 285.483/Binding site: carbohydrate (Asn) (covalent) #status predicted
F. 14-466, 52-277, 64-76, 139-473, 281-305/Disulfide bonds: #status predicted
F. 539, 546, 549/Binding site: palmitate (Cys) (covalent) #status predicted
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                                                                                                                                                                                - influenza A virus (strain A/swine/126/82) (fragment)
                                                                                                                                                                                                     C;Species: Influenza A virus
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 18-Sep-1998
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as Glu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 1;
Pred. No. 0.27;
0; Mismatches
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Pred. No. 0.27;
0; Mismatches
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R;Kida, H.; Shortridge, K.F.; Webster, R.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.7%;
90.9%;
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90.98;
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SCYPYDVPDYA 106
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C. Species: Influenza A virus (1759mcn.) (1750mcn.) (17
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A;Residues: 1-74, Nv, 76-120, Tr, 122-156, LL, 158-173, Fr, 175-188, Sr, 190-200, Kr, 202-2
A;Cross-references: EMBL:246413; NID:9609059; PIDN:CAA86548.1; PID:9609060
A;Experimental source: isolate A/Scotland/142/93
C;Superfamily: influenza virus hemagglutinin
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A;Rosidues: 1-134, K',136-156, L',158-173, F',175-188, S',190-218, F',220-225, L',227
A;Crosz-references: EMBL:246395; NID:9609027; PIDN:CAA86530.1; PID:91228087
A;Experimental source: isolate A/England/269/93
A;Accession: S52181
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A;Residues: 1-134,'K',136-156,'L',158-173,'F',175-188,'S',190-218,'F',220-225,'L',227
A;Cross.references: EMBL:246399; NID:9609035; PIDN:CAA86534.1; PID:9609036
A;Experimental source: isolate A/England/328/93
A;Accession: S52194
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A;Residues: 1-134, K',136-156,'L',158-173,'F',175-188,'S',190-218,'F',220-225,'L',227
A;Cross.references: EMBL:246414; NID:g609061; PIDN:CAA86549.1; PID:g609062
A;Experimental source: 1solate A/Scotland/160/93
A;Accession: S52196
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A; Residues: 1-74, N', 76-120, T', 122-156, 'L', 158-173, 'F', 175-188, 'S', 190-200, 'K', 202-2
A; Cross-references: EMBL: 246402; NID: 9609041; PIDN: CAA86537.1; PID: 9609042
A; Experimental source: 1solate A/England/471/93
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A;Variety: isolate A/Beljing/353/89
C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 20-Sep-1999
C;Accession: S52174
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A;Residues: 1.347 <EL3>
A;Cross-references: EBL:Z46409; NID:g609057; PIDN:CAA86544.1; PID:g609058
A;Experimental_source: isolate A/Hong Kong/34/90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:246410; NID:g609053; PIDN:CAA86545.1; PID:g609054
A;Experimental source: isolate A/Hong Kong/23/92
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Best Local Similarity luv...
Fra 9; Conservative
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A; Residues: 1-347 <EL2>
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C; Species: influenza A virus
C; Species: influenza A virus
C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C; Accession: J02378
R; Rocha, E.P.; Xu, X.; Hall, H.E.; Allen, J.R.; Regnery, H.L.; Cox, N.J.
J; Gen. Virol. 74, 2513-2518, 1993
A; Title: Comparison of 10 influenza A (H1N1 and H3N2) haemagglutinin sequences obtained
A; Reference number: J02369; MUID:94065682
A; Accession: J02378
A; Molecule type: mRNA
A; Residues: 1-331 < ROC>
A; Cross-references: GB:L20102
A; Experimental source: subtype H3N2
C; Superfamily: influenza virus hemagqlutinin
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C)Species: influenza A virus
C)Bate: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: J02377
C;Accession: J02377
C;Accession: J02377
C;Accession: J02369; Mulb: 4-L: Allen, J.R.; Regnery, H.L.; Cox, N.J.
J. Gen. Virol. 74, 2513-2518, 1993
A;Title: Comparison of 10 influenza A (HINI and H3N2) haemagglutinin sequences obtained A;Reference number: J02369; Mulb: 94065682
A;Accession: J02377
A;Molecule type: mRNA
A;Residues: 1-331 <ROC>
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0.23;
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                                                                 A Molecule type: mRNA
A; Residues: 1-330 < ROC>
A; Cross references: GB:L20119
Experimental source: subtype H3NZ
C; Superfamily: influenza virus hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross references: GB:L20105
A:Experimental source: subtype H3N2
C;Superfamily: influenza virus hemagglutinin
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1larity 100.0%; Pred. No.
Conservative 0; Mismatci
A; Reference number: JQ2369; MUID: 94065682
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Best Local Similarity 100.0
درم 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Cyaccession: S52178
R;Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circ A;Reference number: S52178
A;Accession: S52178
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A:Variety: influenza A virus
A:Variety: isolate A/England/286/93
C:Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C:Accession: 552179
R:Ellis, J.S.
submitted to the EMBL Data Library, October 1994
A:Pescription: Antigenic and genetic variation in the haemagglutinin of recently circ A:Reference number: 552173
A:Accession: 552179
                                                                                                                                                                                                     hemagglutinin – influenza A virus (isolate A/England/284/93) (fragment) C;Species: influenza A virus Species: influenza A virus A A.Variety: isolate A/England/284/93 C;Date: 07-May-1995 %sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
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A; Rocsidues: EMBL:Z46396; NID:g609029; PIDN:CAA86531.1; PID:g609030
A; Experimental source: isolate A/England/284/93
C; Superfamily: Influenza virus hemagglutinin
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Pred. No. 0.24;
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Pred. No. 0.24;
0; Mismatches
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A; Residues: 1-347 <ELL>
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C;Spezis influenza A virus (isolate A/England/1/93) (fragment)

C;Speziety: isolate A/England/1/93

C;Date: 07-May-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001

C;Accession: $52175

S;Bilis, J.S.

Submitted to the EMBL Data Library, October 1994

A;Bescription: Antigenic and genetic variation in the haemagglutinin of recently circula

A;Accession: $52175

A;Andlecule type: mRNA

A;Reference number: $52173

A;Andlecule type: mRNA

A;Residues: 1-347 <ELL:
A;Cross-references: EMBL:Z46393; NID:g609024; PIDN:CAA86528.1; PID:g940547

A;Experimental source: isolate A/England/1/93

C;Superfamily: influenza virus hemagglutinin
Riellis, J.S.
submitted to the EMBL Data Library, October 1994
submitted to the EMBL Data Library, October 1994
Arbescription: Antigenic and genetic variation in the haemagglutinin of recently circula ArBeference number: S52173
Arcession: S52174

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A;Variety: isolate A/England/247/93
A;Variety: isolate A/England/247/93
A;Variety: isolate A/England/247/93
C;Species: OrMay-1995 #sequence_revision 23-Feb-1996 #text_change 23-Mar-2001
C;Accession: S52176
B;Ellis, J.S.
Submitted to the EMBL Data Library, October 1994
A;Description: Antigenic and genetic variation in the haemagglutinin of recently circula A;Reference number: S52173
A;Accession: S52176
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/68 (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-!- FUNCTION: HERAGGLOTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISCULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEMAGGLUTININ HAI CHAIN.
HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                   P17001
P17001
P17002
P26134
P26141
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P12586
 P16998
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Q08011
                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-NOV-1995 (Rel. 40, Last annotation update)
10-NG-2001 (Rel. 40, Last annotation update)
10-NG-2011 RECURSOR (CONPAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Influenza A virus (strain A/Duck/Hong Kong/7/75).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIROLOGY 162:160-166(1988).
-!- FUNCTION: HERAGGLOTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kida H., Shortridge K.F., Webster R.G.; "Origin of the hemagglutinin gene of H3N2 influenza viruses from pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                        Gaps
                                                                                                                                                                                           HEMA_IAZH3 STANDARD; PRT; 550 AA.
P1134; Q84025; Q84026;
01-201-1999 (Rel. 11, Created)
01-JUL-1999 (Rel. 11, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ
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W; 991F6D8BCO2F24F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                   Influenza A virus (strain A/Swine/Hong Kong/126/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
NCBL_TaxID=11498;
                      Indels
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                      0; Mismatches
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HSSP: P03437; 2HMG.
InterPro; IPR001364; Hemagglutn.
Pfan; PP00509; Hemagglutin; 1.
ProDom; PD000225; Hemagglutn; 1.
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90.98;
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  Best Local Similarity
                                                                                                                                                                                                                                                                                                                    CHAIN] (FRAGMENT).
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89204899; PubMed-2705299;
Kawaoka Y., Bean W.J., Webster R.G.;
"Evolution of the hemagglutinin of equine H3 influenza viruses.";
Virology 169:283-292(1989).
-! FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-! SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISCLEIDE BOND.
-! SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
20-bug-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECHSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 565;
                                                                                                                                                                                                                                                                                                                                                       Influenza A virus (strain A/Equine/Kentucky/2/86).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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InterPro; IPR001364; Hemaggluth.
Pfam: PF00509; Hemaggluthin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
PRINTS; PR00330; HEMAGGLUTN1.
PRINTS; PR00331; HEMAGGLUTN1.
PRODOM; PR000225; HEMAGGLUTN2.
Probom; P000225; Hemaggluth; 1.
Envelope protein; Hemaggluthin; Glycoprotein; Signal.
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2038CC1C6C9B88C5 CRC64;
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HEMAGGLUTININ HA2
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Pred. No. 0.086;
565 AA
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PIR; A34065; HMIVET.
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         STANDARD;
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 9; Conserv
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
-i- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
-i- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sleigh M.J., Both G.W., Underwood P.A., Bender V.J.; "Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAI CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 55; DB 1; Length 320;
Pred. No. 0.072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Ou/7/70).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9C3A86B3A8D856FE CRC64;
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N-LINKED (GLCNAC...
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InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutfini, 1.
Propom; P0000225; Hemagglutni; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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100.0%; Pred. No. v.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      328 HE 8 N - 22 N - 38 N - 63 N - 63 N - 2165 N - 328 N - 328 N - 36072 MW;
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Best Local Similarity
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                                                                                                                                                                                                                               Gething M.-J., Bye J., Skehel J.J., Waterfield M.;

Gething and DNA sequence of double-stranded copies of haemagglutinin genes from H2 and H3 strains elucidates antigenic shift and drift in human influenza virus.";

Nature 287:301-306(1980).

-! FUNCTION: HERMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-! SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAA AND HA2) LINKED BY A DISULFIDE BOND.

-! SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

PIR: A04051: HMIVH.
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13-AUG-1987 (Rel. 05, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ [CONTAINS: HEMAGGLUTININ HAI CHAIN] (FRAGMENT).
    20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%; Score 55; DB 1; Length 249; 100.0%; Pred. No. 0.055;
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
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                                                                             Influenza A virus (strain X-31).
Viruses; ssRNA negative-strand viruses; Orthomyxovi
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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ProDom; PD000225; Hemagglutn; 1.
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20-AUG-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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P03441; Q83961; Q83962;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HAI CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%; Score 55; DB 1; Length 328; 100.0%; Pred. No. 0.072; 1.ve 0; Mismatches 0; Indels
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Viruses: ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                       MW; E30A962FD6DD805B CRC64;
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          Envelope protein; Hemagglutinin; Glycoprotein.
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InterPror; IPRO01364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INTITATING INFECTION.

-!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HAZ) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HA2 CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEMA_IADH1 STANDARD; PRT; 550 AA.
P12582; Q84021; Q84022;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-0198 (Rel. 12, Last sequence update)
01-OCT-0101 (Rel. 10, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HA1 CHAIN; HEMAGGLUTININ HA2 CHAIN)
                                                                                                                                                                                                                         Length 550;
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                                                                                        0; Indels
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InterPro; IPR001364; Hemagglutn.
Pfan; PF00509; Hemagglutinin; 1.
ProDom; P0000225; Hemagglutni; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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nes 9; Conservative
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HEMA_IADH4
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-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITITATING INFECTION.

-I- SUBUNIT: HOMOTIMER. BACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISCLEIDE BOND.

-I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HAZ CHAIN.

N-LINKED (GLCNAC...) (POTENTIAL).

K -> N (IN PIR DATA BANK).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-STA565458, PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                              ;
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                                                                                                                                                           HEMA_IADH2 STANDARD; PRT; 550 AA.
1912881, 084011;
01-0CT-1999 (Rel. 12, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAZ CHAIN), HEMAGGLUTININ HAZ CHAIN)
   Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 550;
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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   DB 1;
0.12;
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Probom; PD000225; Hemagglutin; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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0.12;
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                               Mismatches
73.3%; Score 55;
100.0%; Pred. No.
ive 0; Mismatch
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Best Local Similarity
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-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-I- SUBUNIT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-I- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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HEMAGGLUTININ HA2 CHAIN.
N-LINED (GLCNAC. . .) (POTENTIAL).
M-LINED (GLCNAC. . .) (POTENTIAL).
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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1912585; 084013; 084014;
01-0cT-1989 (Rel. 12, Created)
01-0cT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annoctation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
HEVA_IADH3 STANDARD; PRT; 550 AA.
P12584; Q84012; Q89793;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEWAGGLUTININ PRECURSOR [CONTAINS: HEWAGGLUTININ HAI CHAIN; HEWAGGLUTININ HAZ CHAIN] (FRAGMENT).
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Pfam; PF00509; Hemagglutinin; 1.
Probom; PD000225; Hemagglutinin; 1.
Envelope protein; Hemagglutinin; 6lycoprotein.
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                                                                                                                                                      -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
-1- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
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                                                                            SEQUENCE FROM N.A.
MEDILINE-87265458; PubMed-2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87265458; PubMed=2440178;
Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 550;
             VIruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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 Influenza A virus (strain A/Duck/Hokkaido/7/82).
                                                                                                                                                                                                                                                                                                                                                                               Pfan; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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Pred. No. 0.12;
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100.0%; Pre
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550 AA;
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                                                    NCBI_TaxID=11360;
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HEMA_IADH6
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                    -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.
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-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INITIATING INFECTION.

-!- SUBUNT: HOWOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                         -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
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Kida H., Kawaoka Y., Naeve C.W., Webster R.G.;
"Antigenic and genetic conservation of H3 influenza virus in wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                           -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 550;
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Influenza virus A and B group; Influenza A viruses;
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Pfam; PF00509; Hemagglutinin; 1.
Probom; P0000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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Virology 159:109-119(1987).
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Pfam; PF00509; Hemagglutinin; 1.
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Best Local
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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                                                                                                                                                              HEMAGGLUTININ HAI CHAIN.
HEMAGGLUTININ HAZ CHAIN.
N-LINED (GLCNAC. . .) (POTENTIAL).
W; GEF81793281D53EB CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HEMAGGLUTININ HECUREOR [CONTAINS: HEMAGGLUTININ HAI CHAIN; HEMAGGLUTININ HAZ CHAIN]
                                                                                                                                                                                                                                                                                               Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strain A/Duck/Hong Kong/64/76).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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0.12;
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                                                                                                      InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
ProDom; PD000225; Hemagglutn; 1.
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                                                                                 EMBL; M16743; AAA43149.1; -.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                             G27813; HMIV15.
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P43258;
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InterPro; IPR001364; Hemagglutn

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Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda J., Shortridge K.F., Shimizu Y., Kida H.;
Yasuda M.;
Molecular evidence for a role of domestic ducks in the introduction of avian H3 influenza viruses to pigs in southern China, where the A/Hong Kong/GB (H3N2) strain emerged.";
J. Gen. Virol. 72:2007-2010(1991).
-!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO CELL RECEPTORS AND FOR INTIATING INRECTION.
-!- SUBBUIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (HAI AND HA2) LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                                           Gaps
                                                                                 N-LINKED (GLCNAC. . ) (POTENTIAL).
M. A351CS6789E4BE9A CRC64;
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HEMAGGLUTININ HAZ CHAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last annotation update)
HEMAGGLUTININ PRECURSOR (CONTAINS: HEMAGGLUTININ HAI CHAIN;
HEMAGGLUTININ HAZ CHAIN] (FRAGMENT).
                                                                                                                                                                                                                                         Length 550;
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Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
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                                                                     CHAIN
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                                                   HEMAGGLUTININ HAI
HEMAGGLUTININ HA2
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Probom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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0.12;
ProDom; PD000225; Hemagglutn; 1.
Envelope protein; Hemagglutinin; Glycoprotein.
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Pred. No.
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CARBOHYD 483 483 N-LINKED (GLCNAC. .) (POTENTIAL). SEQUENCE 550 AA; 61762 MW; 6FEF8B49488C191A CRC64; FT

ó; 0; Gaps Query Match
Pest Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels

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Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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36562 MW; 9DD1CA9187D537DF CRC64;
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FICCH W.M., Bush R.M., Bender C.A., COX N.J.;
FICC Natl. Acad. Sci. U.S.A. 0:0-0(1997).
EMBL; AF008858; AAB69800.1; -
InterPro; IPRO01364; Hemagglutin.
Probom; PD000225; Hemagglutin: 1.
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Best Local Similarity 90.9
Matches 10; Conservative
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Q9wa90 1
Q9w8z1 1
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Q9w8j7
Q9w126
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Q9w124
Q40774
Q9d145
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Compugen Ltd
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              GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                        protein search, using sw model
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_phage:*
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sp_bacteria:*
sp_fung1:*
sp_human:*
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DEQUENCE FACE in it. 1. STRAIN-A/GUANGDONG/25/93; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; MEDLINE-96105347; PubMed=7503689; Memagglutinin of recently circulating human influenza A (H3N2) viruses in the United Kingdom."; Arch. Virol. 140:1889-1904(1995). EMBL; 246406; CAA86541.1; InterPro; IPRO01364; Hemagglutin. ProDom; PRO0509; Hemagglutinin; 1. ProDom; PD000225; Hemagglutinin; 1.
                                                                                                                                                                                                                                                 ^{1}\mathrm{Evolution} are the transfer of the second human H3N2 influenza A isolates from Japan and China: novel changes in the receptor binding
                                                                                                                                    SEQUENCE FROM N.A.
STRALN-A/CUANDONG/28/94 (H3N2);
MEDLINE-96370797; PubMed-8774633;
Lindstrom S., Sugita S., Endo A., Ishida M., Huang P., Xi S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 12; Length 344; Pred. No. 0.31;
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                                       Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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Influenza virus A and B group; Influenza A viruses.
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SEQUENCE 344 AA; 38139 MW; C5A8CC7DBBOACBAE CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  HAEMAGGLUTININ.
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                                                                                                                                                                                                                                                                                      domain.",
Arch. Virol. 141:1349-1355(1996).
EMBL. 0484422, AABOQ9416.1;
InterPro.; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutnin; 1.
ProDom; PD000225; Hemagglutnin; 1.
CHAIN 17 >344 HAEMA
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90.98;
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    HAEMAGGLUTININ (FRAGMENT)
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Best Local Similarity 90.99
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
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112 SCYPYDVPDYA 122
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Best Local Similarity
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                              Influenza A virus
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SEQUENCE
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Q82787;
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                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-A/HONG_KONG/1/94(H3N2);
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008772; AABG3709.1;
InterPro; IPR001364; Hemagglutn.
Probom; PF00609; Hemagglutnin; 1.
Probom; PF00609; Hemagglutnin; 1.
Probom; PF00609; Hemagglutnin; 1.
NON_TER 1 1
NON_TER 329 AA; 36630 MW; DIDF31668818FA8D CRC64;
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                                                                              Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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Viruses; SRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
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STRAIN-A/GUANGDONG/25/93(H3N2);
STRAIN-A/GUANGDONG/25/93(H3N2);
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF008898; AAB63765.1; -
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutnin; 1.
Probom:
Probom:
PD000225; Hemagglutn; 1.
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329 AA; 36566 MW; 4DD909217213F423 CRC64;
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040820;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HEMAGGLUTININ GENE (FRAGMENT).
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Last annotation update)
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90.98;
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(TrEMBLrel. 02, I
(TrEMBLrel. 17, I
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Best Local Similarity
Matches 10; Conserva
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Matches 10; Conserva
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01-FEB-1997 (
01-JUN-2001 (
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EDUCED FROM N.A.

STRAIN-TOKYO1570, TOKYO1566, TOKYO1567, TOKYO1568, TOKYO1569;
MOTI S., Sekine H.;
MOTI S., Sekine H.;
MIAI domain of Influenza A (H3N2) virus.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB013813; BAA77281.1;
EMBL; AB013810; BAA77288.1;
EMBL; AB013811; BAA77289.1;
EMBL; AB013811; BAA77289.1;
EMBL; AB013811; BAA77289.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%; Score 55; DB 12; Length 236; 100.0%; Pred. No. 0.29; Live 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
STRAIN-TOXY(21527, TOXY(01511;
MOA1 S., Seklie H.; TOXY(01511;
MOA1 S., Seklie H.; TOXY(01511;
MA1 Gonain of Influenza A (H3N2) virus.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB013807; BAA77285.1; ---
EMBL; AB013805; BAA77284.1; ---
InterPro; IPR001364; Hemagglutn.
PERM: PR00539; Hemagglutn.
PRINTS; PR00329; Hemagglutn.; 1.
PRINTS; PR00325; Hemagglutn; 1.
NON_TER
1 1
NON_TER
236 236
SEQUENCE 236 AA; 26477 MW; 4566C8E7210FB558 CRC64;
                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses.
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Influenza virus A and B group; Influenza A viruses.
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                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMRNT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMENT).
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0.29;
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Best Local Similarity 100.
Matches 9; Conservative
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Q9W8Z1;
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Q9W8T9
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                                                                                                                                                                                                                                                                                                   SEUENCE FROM N.A.
STRAIN-A/HONG KONG/2/94;
STRAIN-B/HONG KONG/2/94;
STRAIN-B/HONG KONG/2/94;
STRAIN-B-96105347; PubMed-7503689;
Ellis J.S., Chakraverty P., Clewley J.P.;
Ellis J.S., Chakraverty P., Clewley J.P.;
Genetic and antigenic variation in the haemagglutinin of recently
circulating human influenza A (H3N2) viruses in the United Kingdom.";
Arch. Virol. 140:1889-1904 (1995).
EMBL; 246408; CAA6633.1; ...
InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
Propom; P0000225; Hemagglutn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4), COMPLETE CDS.
Influenza A virus (strain A/Equine/Kentucky/2/86).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
1N-LUN-2001 (TrEMBLRel. 17, Last annotation update)
1NFLUENZA A/EQUINE/KENTUCKY/2/86 (H3N8) HEMAGGLUTININ (HA) RNA (SEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=89204899; PubMed=2705299;
Kawaoka Y., Bean W.J., Webster R.G.;
Fevolution of the hemagglutinin of equine H3 influenza viruses.";
Virology 169:283-292(1989).
InterPro: IPRO01364; Hemagglutin.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTINI2.
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                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
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CHAIN 1 344 POTENTIAL.
CHAIN 345 565 POTENTIAL.
SEQUENCE 565 AA; 63592 MW; EB9FEFF7CBB861DB CRC64;
                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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347 AA.
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PRT;
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                                                                                                                                          HAEMAGGLUTININ (FRAGMENT).
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Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
PRELIMINARY;
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109 SSNCYPYDIPDYA 121
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SEQUENCE FROM N.A.
STRAIN=A/TAINWAN/2192/96;
Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Shih S.-R., Chen S.-H., Wu S.-L., Ho G.-C.;
"Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    influenza A virus (A/Taiwan/2192/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenza A virus (A/Taiwan/2191/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Unfluenza a virus A and B group; Influenza A viruses; Influenza A virus.
NCBL_TaxID-95236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.3%; Score 55; DB 12; Length 286; 100.0%; Pred. No. 0.36; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             Indels
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF139937; AAD34854.1; -.
InterPro; IPR001364; Hemagglutin.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTNI2.
ProDom; PD000225; Hemagglutn; 1.
NON_TER 1 1 1 1 1 1 NON_TER 286 SEQUENCE 286 AA; 32075 MW; 7BA39C7632D33186 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF139936; AAD34053.1; -. InterPror; IPR001364; Hemagglutn. Pfam; PF00509; Hemagglutninin; 1. PRNINTS; PR00329; HEMAGGLUTN12.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
H3 HEMAGGLUTININ (FRAGMENT).
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100.0%; Pred. No. 0.36;
ative 0; Mismatches 0
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NON_TER 1 1
NON_TER 286 286
SEQUENCE 286 AA; 32059 MW; C
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Best Local Similarity الاست.
نمر 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Shih S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         influenza A virus (A/Taiwan/2034/96(H3N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza A virus.
NCBI_TaxID=95241;
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"Nati domain of influenza A (H3N2) virus.";
"Nati domain of influenza A (H3N2) virus.";
"Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.";
"EMBL, AB014061; BAA77294.1; -...
"EMBL; AB013808; BAA77292.1; -...
"EMBL; AB014060; BAA77292.1; -...
"EMBL; AB014061; BAA77293.1; -...
"InterPro; IPR001364; Hemagglutin."
"Pfam; PF00569; Hemagglutin."
"Pfam; PF00569; Hemagglutin."
"Pfam; PF00569; Hemagglutin."
"Pfam; PF00569; Hemagglutin."
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                                                                                                                                                                                                                                                                                                             Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBL_TaxID=11320;
           Indels
                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
STRAIN-72, 70, AND 71;
Nagashima M., Mori S., Sekine H.;
"Influenza A virus gene for hemagglutinin.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ (FRAGMENT).
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Last sequence update)
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           Mismatches
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       9; Conservative
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Best Local Similarity
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                                                              11 YPYDVPDYA 19
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                                           5 YPYDVPDYA 13
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SEQUENCE
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         Matches
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SEQUENCE FROM N.A.
STRAIN-A/FINLAND/583/98;
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SEQUENCE FROM N.A.
STRAIN-A/TAIWAN/2191/96;
Shin S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Shin S.-R., Chen S.-H., Wu S.-L., Ho C.-C.;
Sequence Analysis of HA and NA Genes of Influenza Viruses Isolated in Taiwan.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF139332; AAD34849.1;
EMBL: AF139332; Hemagglutin.
Pfam: PF00509; Hemagglutinin: 1.
PRINTS: PR00329; Hemagglutinin: 1.
Prodom: PD000225; Hemagglutin: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
NCBI_TaxID=11320;
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SERAIN-A/ILLINOIS/5/95(H3NZ);
Fitch W.M., Bush R.M., Bender C.A., Cox N.J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF008782; AAB63719.1;
InterPro; IPR001364; Hemagglutin.
Pfam; PF00509; Hemagglutinin; 1.
Probom; PD000225; Hemagglutn; 1.
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                                                                                                                                                                                                                                                                                                                                     286 AA; 31976 MW; 69AB2AE727D26078 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEMAGGLUTININ GENE (FRAGMENT).
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.3
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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RC STRAIN-AP/FINLAND/S81798;
RA Pyhala R., Haanpaa M., Kleemola M., Tervahauta R., Visakorpi R.,
RA Kinnunen L.;
RA Kinnunen L.;
RA Kinnunen L.;
RA Kinnunen L.;
RE Kinnunen L.;
RI "Acceptable protective efficacy of influenza vaccination in young
RT military conscripts in circumstances of incomplete antigenic and
RT genetic match.;
RI Vaccine (0.012001).

DR EMBL; AF311689; AA647810.1; -
DR EMBL; AF311689; AA647810.1; -
DR PRINTS; PRO0329; Hemagglutn.
DR PRINTS; PRO0329; Hemagglutn.
DR PRINTS; PRO0329; Hemagglutn.
DR PRINTS; PRO0329; Hemagglutn.; 1.
DR PRODOM:
PT NON_TER 325
SEQUENCE 325 AA; 36029 MW; 5BECB8CC3E83B1C2 CRC64;

Query Match
Rest Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YPYDVPDYA 13

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| Db 98 YPYDVPDYA 13
| Search completed: April 11, 2002, 10:22:57
Job time: 477 sec
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